****	(TM)	*****
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:34:45 2000; MasPar time 7.31 Seconds 505.226 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-016-869A-2 (1-136) from US09016869A.pep 1078 1 MDPAAGSSMEPSADWLATAA......TRGSNHARIDAAEGPSDIPD 156 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 segs, 23686106 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq36 1:geneseqp

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.169; Variance 144.272; scale 0.216

SUMMARIES

		æ			CHINAMA		
Result No.	Score	Query	Query Match Length DB	98	OI OI	Description	Pred. No.
п	1078	100.0	156	-	R85116	Cell-cycle regulatory	1.18e-85
7	1067	99.0	156	Н	W80524	A human multiple tumou	1.20e-84
٣	1067	99.0	156	Н	W40524	Human MTS1 protein.	1.20e-84
4	1067	99.0	156	-	W74549	Amino acid sequence of	1.20e-84
S	1067	99.0	156	-	W19251	Human multiple tumour	1.20e-84
ø	1067	99.0	156	Н	W10627	Tumour suppressor pl6.	1.20e-84
7	1064	98.7	391	-	W95094	Human p27-p16 fusion p	2.26e-84
80	1064	98.7		-	W23534	CDK inhibitory fusion	2.26e-84
σ	1057	98.1		Н	W95105	Truncated p27/p16 fusi	9.86e-84
10	1057	98.1		-	W95106	Truncated p27/p16 fusi	9.86e-84
11	1057	98.1		ч	W95103	Truncated p27/p16 fus1	9.86e-84
12	1057	98.1		-	W23536	CDK inhibitory fusion	9.86e-84
13	1057	98.1		Н	W95096	Human p16p27 fusion pr	9.86e-84
14	1057	98.1		٦	W95107	Human p16p27 fuston pr	9.86e-84
15	1057	98.1		-	W95095	p27 fus	9.86e-84
16	1057	98.1		Н	W23535	CDK inhibitory fusion	9.86e-84
17	1056	98.0		Н	W19252	Human multiple tumour	1.22e-83
18	1050	97.4		Н	W19253	Human multiple tumour	4.31e-83
19	1037	96.2	348	٦	W95104	Truncated p27/p16 fus1	6.65e-82
20	1030	95.5		, -1	R81701	Multiple tumour suppre	٠
21	1030	95.5	148	Н	R80940	Human multiple tumour	2.90e-81
22	1030	95.5		ч	R53401	Inhibitor of cyclin de	2.90e-81
23	921	85.4	157	П	R85114	Cell-cycle regulatory	2.59e-71

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1.33e-54	2.02e-54	2.02e-54	2.02e-54	2.02e-54	2.02e-54	2.02e-54	7.06e-54	1.62e-53	1.62e-53	1.62e-53	1.62e-53	1.62e-53	1.62e-53	1.97e-52	4.31e-49	2.58e-38	6.67e-32	6.31e-31	6.31e - 31	1.54e-28	1.54e-28
Cell-cycle regulatory	Amino acid sequence 1	Human multiple tumour	Human multiple tumour	Human MTS1E1-beta prot	Multiple tumour suppre	A human multiple tumon	Mouse multiple tumour	Human multiple tumour	A human multiple tumou	Multiple tumour suppre	Amino acid sequence 2	Human MTS2 protein.	Human multiple tumour	Cell-cycle regulatory	Mouse multiple tumour	Cell-cycle regulatory	Human INK4a-p16 C-term	O)	Cell-cycle regulatory		
R85118	W74550	R80947	W19254	W40525	R81700	W80525	W70823	R80948	W80526	R81702	W74553	W40526	W19255	R85117	W80527	R85115	W16324	W16322	R85120	R85113	R85119
٦	-	н	Н	Н	Н	н	-	-	н	н	Н	н	Н	Н	ч	ч	Н	н	Н	н	Н
130	105	105	105	105	105	105	130	138	138	138	138	138	138	138	168	138	67	125	125	82	127
68.4	68.2	68.2	68.2	68.2	68.2	68.2	67.6	67.3	67.3	67.3	67.3	67.3	67.3	66.1	62.7	51.6	44.9	43.9	43.9	41.4	41.4
737	735	735	735	735	735	735	729	725	725	725	725	725	725	713	9/9	556	484	473	473	446	446
24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT	
a	R85116 standard; Protein; 156 AA.
ğ	R85116;
딥	01-MAR-1996 (first entry)
DE	p16.
KK	cycle re
ΚW	CCR; cancer; cell proliferation.
SO	sapiens.
PN	WO9528483-A1.
PD	26-OCT-1995.
PF	14-APR-1995; U04636.
PR	14-APR-1994; US-227371.
PR	25-MAY-1994; US-248812.
P.R	
PR	
PA	OLD SPRING HARBOR LAB.
PI	Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
DR	WPI; 95-373798/48.
DR B	N-PSDB; T02962.
ᅜ	New cell cycle regulating proteins bind to cyclin dependent kinase -
ď	and related nucleic acids, antibodies etc., used in diagnosis and
딥	therapy of abnormal cell proliferation, degeneration etc.
PS	Claim 1; Page 76-77; 109pp; English.
႘	The human cell-cycle regulatory (CCR) protein p16 (R85116) was
ខ	obtd. by expression of a cDNA clone (T02962) isolated in a 2-hybrid
ပ္ပ	screening assay. CCR p16 specifically inhibits the activity of
႘	cyclin-dependent kinases during various stages of the cell cycle,
႘	and can be used in the treatment and diagnosis of proliferative
ပ္ပ	disorders.
ÖS	Sequence 156 AA;
ē	
2 6	Vect. Advantage 10.08: Pred. No. 1.188-85:
Ma	
a a	1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVAMAGSARVA 60
οχ	1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQYMMMGSARVA 60
ı	
a a	61 ELLILHGAEPNCADPATLTRPVHDAAREGFIDTLVVLHRAGARLDVRDAMGRLPVDLAEE 120
δ	61 ELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ELLLIHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NA Specific for Multiple Tumour Suppressor IEI-beta gene - are useful for the diagnosis of cancers related to MTSIEI-beta mutation(s) and their treatment bisclosure; Column 63-64; 72pp; English.
This sequence represents a human multiple tumour suppression protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoms, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Columns 65-66; 80pp; English.

The present sequence represents a human multiple tumour suppressor (WTG1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design
                                                                                                                                                                                                 01-DEC-1998.
28-JUL-1995; 058735.
28-JUL-1995; uS-508735.
07-JUN-1995; uS-487033.
(MYRI-) MYRAAD GENETICS INC.
Jiang P., Kamb A, Stone S;
WPI; 99-044585704.
N-PSDB; V70583.
MOUSE multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1067; DB 1; Length 150
Pred. No. 1.20e-84;
1; Mismatches 1; Indels
                                                    03-FEB-1999 (first entry)
A human multiple tumour suppressor 1 (MTS1) protein.
Human; multiple tumour suppressor 1 gene; MTS1; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W40524 standard; Protein; 156 AA.
W40524;
W80524 standard; Protein; 156 AA.
W80524;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.7%;
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995; 487033.

07-JUN-1995; US-487033.

18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-JUN-1994; WS-227369.
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WPI: 98-250421/22.
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N-PSDB; V11238
                                                                                                                                                  Homo sapiens.
US5843756-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      design
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mutation(s)

Successive the authorists and treatment of convers retrieved to mutation(s)

This is the amino acid sequence of the multiple tumour suppressor I this is the amino acid sequence of the multiple tumour suppressor I this is the amino acid sequence of the multiple tumour. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for secen for drugs to be used for cancer therapy, and the protein scene for drugs to be used for cancer therapy, and the protein selection in a cell.
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MTS1. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosts of predisposition to cancers. e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
                                                                                                                                                                                                                                                                                                       1 MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVA 60
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04-DEC-1998 (first entry)
Amino acid sequence of multiple tumour suppressor 1.
Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
somatic mutation; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                1 MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVA
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                                                                                                                                                   Length 156;
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                                                                                                                                                     Score 1067; DB 1; Length 15
Pred. No. 1.20e-84;
1; Mismatches 1; Indels
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W74549 standard; Protein; 156 AA.
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Best Local Similarity 98.7%;
Matches 154; Conservative
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07-UN-1995; 480810.

07-UN-1995; 480810.

18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-UN-1994; US-227369.
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WO9906540-A2.
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Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;

Cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
anti-angiogenic activity; hyperproliferative disorder.

Homo saplens.

W09703635-A2.
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                                    61 ELLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE
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                                                                                                                                                                                                                                                                                         Human multiple tumour suppressor 1 gene product.
Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s) Claim 1; Columns 61-64; 72pp; English.
The present sequence the human multiple tumour suppressor 1 (MTS1) gene product, useful in cancer diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.0%; Score 1067; DB 1; Length 156; larity 98.7%; Pred. No. 1.20e-84; Conservative 1; Mismatches 1; Indels
                                                                                                                     121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                 LGHRDVARYLRAAGGTRGSNHARIDAAEGPSDIPD
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                                                                                                                                                                                                                          standard; Protein; 156 AA.
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18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215086.
14-APR-1994; US-227369.
01-JUN-1994; US-227369.
07-JUN-1995; WO-UG3537.
07-JUN-1995; US-A74177.
(MYRI-) MYRIAD GENETICS INC.
(UTAH ) UNIV UTAH RES FOUND.
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17-JUL-1995; US-502881.
(TEXA ) UNIV TEXAS SYSTEM.
JIN X, ROLH J;
WPI: 97-133336/12.
N-PSDB; TG0951.
                                                                                                                                                                                                                                                               10-SEP-1997 (first entry)
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Best Local Similarity
Matches 154; Conser
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N-PSDB; T72311
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W19251
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Expression construct contg. DNA for tumour suppressor p16 - to restore p16 activity to transformed cells, useful for treating lung or bladder cancer or melanoms.

To bladder cancer or melanoms.

This sequence represents the tumour suppressor p16. The DNA encoding this sequence is joined to a promoter functional in enkaryotic cells and used in the expression construct of the invention. p16 is an inhibitory subunit, which is involved in the control of cyclin-dependent kinase 4 activity, and functions as a tumour suppressor. By detecting this sequence or the DNA encoding it, cancer cells can be detected. When the nucleic acid molecule is in the sense orientation, the expression construct can be used to restore p16 function in a cell, particularly by reversing the transformed phenotype in tumours, especially lung or bladder cancer or melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the nucleic acid molecule is inserted in the antisense orientation, the capression construct inhibits p16 function. Reduced or increased levels of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
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Human p27-p16 fusion protein.
Cyclin-dependent kinase, CDK, CDK/cyclin complex; inhibitory; restenosis;
Cyclin-dependent kinase, CDK, CDK/cyclin complex; inhibitory; restenosis;
CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
intracellular; transcellular; transcytosis; vascular wound; repair; hair;
smooth muscle; cardiovascular; arterlosclerotic; fibrotic disorder;
cellular proliferation; rheumatchd arthritis; diabetes; cirrhosis; graft;
tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
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Claim 63; Page 70-72; 88pp; English.

Claim 63; Page 70-72; 88pp; English.

Claim 63; Page 70-72; 88pp; English.

CDKs), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at Least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVA 60
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29-JUL-1998; U15759.
29-JUL-1997; U5-902572.
(MITO-) MITOTIX INC.
Bach Dh. Gyurls J, Lamphere L;
WPI: 99-153770/13.
N-PSDB; X26220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tachycardia; human; p27; p16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.0%;
Best Local Similarity 98.7%;
Matches 154; Conservative
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delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (1) a therapeutic collyppide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (11) a transcellular consists of at least one CDF-binding motif and a TCP. (A) are used to treat vascular wounds that involve a break in the endothelium and excessive proliferation of smooth muscle, particularly restenosis but core spencially any repair of cardiovascular damage, arteriosclerotic escions or for endothelialisation of synchiat vascular grafts. More generally, FP are used to treat unwanted cellular proliferation in a very wide range of situations, e.g. for treating vascular diseases as above; throris disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many tumours (gliomas, leukaemias); chronic inflammation; neurodegeneration; cane; also to control hair growth (e.g. to prevent hair loss caused by chemotherapy or radiation); periodortal disease; to treat tachycardia; to inhibit spermatogenesis etc. Chimaeric proteins comprising CDK-binding coulisits from two or more different proteins bind to CDRs so inhibit cell cycle progression, particularly smooth muscle cell proliferation. The gene constructs may also be used to produce FP in cell cultures, for production or for regulating cell differentiation in vitro. The present sequence represents a human p27-pl6 fusion protein.
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236 MQRAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 295 296 ELLLIHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 355 121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156 356 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 391 윱 ద ò 셤 ö à

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This sequence represents a chimeric polypeptide of the invention. It was derived from a fusion of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the invention have cyclin-dependent kinase (CDK) binding motifs from at least two different proteins that bind to CDKS. The protein controls proliferation and/or differentiation of cells,
                                              16-MAR-1998 (first entry)
CDK inhibitory fusion protein #1.
Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;
chimeric polypeptide; human; binding motif; proliferation control;
cell differentiation; cell-cycle inhibitor; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                          Chimeric inhibitor of cyclin dependent kinase - useful for gene therapy of cancer and other proliferative and differentiative diseases
                                                                                                                                                                                                                                           /note= "(Gly4Ser)2 linker"
                                                                                                                                                                                                     note- "poly-His tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 40; Page 38-40; 58pp; English.
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                         31-JUL-1997.
17-JAN-1997; 000569.
23-JAN-1996; US-58981.
(MITO-) MITOTIX INC.
Beach D. Gyuris J, Lamphere L;
WPI: 97-393665/36.
N-PSDB; T74051.
                W23534 standard; Protein; 391 AA. W23534;
                                                                                                                                      tissue degeneration; therapy
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                                                                                                                                                                                                                         Misc_difference 205
                                                                                                                                                                                       Misc_difference
                                                                                                                                                                                                                                                             WO9727297-A1.
                                                                                                                                                        Homo sapiens.
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particularly they inhibit cell-cycle progression. They can be used to treat a wide range of proliferative disorders, e.g. cancer, leukaemia, psorlasis, atherosclerosis, restenosis, chronic inflammation etc. They can also treat diseases associated with de-differentiation or degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's diseases, gastric ulcers and autonomous diseases of the peripheral nervous system. Other applications include reducing growth of hair and protecting hair follicle cells against cytotoxic treatments, cosmetically to treat various forms of folliculitis, and to inhibit spermatogenesis or cogenesis. The chimeric proteins can also be used in vitro to maintain cells, especially neurons intended for testing specific activity of trophic factors, at selected points in the cell cycle. The protecting are more active inhibitors of the CDK/cyclin complex than binding motifs used individually (since they may bind to CDK involved in different stages of the cell cycle) Sequence 391 8888888888888888888

0; Gaps Query Match 98.7%; Score 1064; DB 1; Length 391; Best Local Similarity 98.7%; Pred. No. 2.26e-84; Matches 154; Conservative 1; Mismatches 1; Indels

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236 MQRAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVA 295 296 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 355 셤 ò 셤 ö

T 9 W95105 standard; Protein; 237 AA.

356 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 391

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25-MAY-1999 (first entry)
Truncated p27/pl6 fusion protein.
Truncated p27/pl6 fusion protein.
Cyclin-dependent kinase; CDK, CDK/cyclin complex; inhibitory; restenosis; Cyclin-dependent kinase; CDK, CDK/cyclin complex; inhracellular; candothalialisation; fusion protein; therapeutic; acne; intracellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated. Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers, (MITO-) MITOTIX INC.
Beach DH, Gyuris J, Lamphere L;
WPI; 99-153770/13. 29-JUL-1998; U15759. 29-JUL-1997; US-902572. N-PSDB; X26233 Homo sapiens. 11-FEB-1999

differentiation, 101 teacher of, e.g., vascular injury, cancers, claim 63; Page 85; 88pp; English.

Claim 63; Page 85; 88pp; English.

The invention relates to novel inhibitors of cyclin-dependent kinases (TDKs), particularly CDK/cyclin complexes. It provides a recombinant cransfection system (A) that comprises: (1) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at last one CDK-binding motif for binding and inhibiting activity of a CDK, inked to a transcription regulator functional in eukaryotic cells; (11) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (111) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (1) a therapeutic collypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (11) a transcellular process when FP enters the cell, and (11) a transcellular process when FP enters transcytosis of FP. The FP

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binding motif - used for regulation of cell proliferation and
differentiation, for treatment of, e.g. vascular injury, cancers,
fibrosis and neurodegeneration

Fibrosis and neurodegeneration

Claim 63; Page 85; 88pp; English.

Claim 63; Page 85; 88pp; English.

Claim 63; Page 85; 88pp; English.

Comprising a sequence encoding a complexes. It provides a recombinant

Comprising a sequence encoding an inhibitory polypeptide containing at
comprising a sequence encoding an inhibitory polypeptide containing at
comprising a sequence encoding an inhibitory polypeptide containing to
comprising a sequence encoding an inhibitory polypeptide containing to
comprising a tusion metal for binding and inhibiting activity of a CDK,
linked to a transcription regulator functional in eukaryotic cells; (ii)
second gene construct comprising a sequence encoding a polypeptide that
concess endothelialisation, and (iii) a gene delivery composition for
delivering the GCs to a cell for transfection. Also provided are nucleic
collypeptide sequence (TP) from an intraccillular protein that alters a
cellular process when FP enters the cell, and (ii) a transcellular
collypeptide sequence (TP) from an intraccillular protein that alters
consists of at least one CDK-binding motif and a TCP. See X26220 for
consists of at least one CDK-binding motif and a TCP. See X26220 for
consists of a human truncated p27/pl6 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY 1999 (first entry)
Truncated p27/pl6 fusion protein.
Truncated p27/pl6 fusion protein.
Cyclin-dependent kinase; CDK, CDK/cyclin complex; inhibitory; restenosis; Cyclin-dependent kinase; CDK, CDK/cyclin complex; therapeutic; acne; intracellular; transcellularistics; vascular wound; repair; hair; amooth muscle; cardiovascular; arterioscierotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; trachycardia; human; p27; p16; truncated.
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                                                                                                                                                                                                                                                  98 DPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAE 157
                                                                                                                                                                             2 DPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMGSARVAE 61
                                                                                                                        Gaps
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consists of at least one CDX-binding motif and a TCP. See X26220 fo detailed uses of the recombinant transfection system. The present sequence represents a human truncated p27/p16 fusion protein. Sequence 237 AA;
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                                                                                     Length 237;
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Pred. No. 9.86e-84;
                                                                                    Score 1057; DB 1; Length 23
Pred. No. 9.86e-84;
0; Mismatches 1; Indels
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29-JUL-1998; U15759.
29-JUL-1997; US-902572.
(MITO-) MITOTIX INC.
Beach DH, GYULLS J, Lamphere L;
WPI; 99-153770/13.
                                                                                                                                                                                                                                                                                                                                                                                                        W95106 standard; Protein; 252 AA.
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                                                                                    Query Match
Best Local Similarity 99.4%;
Matches 154; Conservative
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Claim 63; Page 83; B8pp; English.

The invention relates to novel inhibitors of cyclin-dependent kinases the invention relates to novel inhibitors of cyclin-dependent kinases (CDKS), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (1) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at last one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (1) second gene construct comprising a sequence encoding a polypeptide that promotes endothellalisation, and (111) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (1) a therapeutic polypeptide sequence (TP) from an intraccillular protein that alters a cellular process when FP enters the cell, and (11) a transcellular collypeptide sequence (TP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and a TCP. See x26220 for detailed uses of the recombinant transfection system. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                         Truncated p27/p16 fusion protein.

Cyclin-dependent kinase, CDK, CDK/cyclin complex; inhibitory; restenosis;
Cyclin-dependent kinase, CDK, CDK/cyclin complex; inhibitory; restenosis;
CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
intracellular; transcellular; transcytosis; vascular wound; repair; hair;
smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
cancellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
tachycardia; human; p27; p16; truncated.
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binding motif - used for regulation of cell proliferation and
differentiation, for treatment of, e.g. vascular injury, cancers,
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Pred. No. 9.86e-84;
                                                                                                                                                 122 GHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                               GHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD
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Beach DH, Gyuris J, Lamphere L;
WPI: 99-153770/13.
N-PSDB; X26231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibrosis and neurodegeneration
                                                                                                                                                                                                                                                                                                                                 W95103 standard; Protein; 334 W95103;
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W23536 standard; Protein; 365
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Best Local Similarity 99.4%;
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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11-FEB-1999.
29-JUL-1998; U15759.
29-JUL-1997; US-902572.
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2 DPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAE 61

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US-09-016-869A-2.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a chimeric polypeptide of the invention. It was derived from a fusion of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the invention have cyclin-dependent kinase (CDK) binding motifs from at least two different proteins that bind to CDKs. The protein controls proliferation addor differentiation of cells, carriarly they inhibit cell-cycle progression. They can be used to particularly they inhibit cell-cycle progression. They can be used to particularly they inhibit cell-cycle progression. They can also treat diseases associated with de-differentiation or confidence of itssue, e.g. Alzheimer's, Parkinson's or Hunington's diseases, gastric ulcers and autonomous diseases of the peripheral nervous system. Other applications include reducing growth of hair and contrast training common include reducing growth of hair and contrast various forms of folliculitis, and to inhibit spermatogenesis or cells, especially neurons intended for testing specific activity of crophic factors, at selected points in the cell cycle. The proteins are more active inhibitors of the CDK-cyclin complex than binding motifs used the contrast than binding motifs used the contrast of the CDK-cyclin complex than binding motifs used the contrast of the CDK-cyclin complex than binding motifs used the contrast of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                            pl6 gene;
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                           16-MAR-1998 (first entry)
CDK inhibitory fusion protein pl6p27.
CDK inhibitory fusion protein pl6p27.
Fusion gene, CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gclimeric polypeptide; human; binding motif; proliferation control; cell differentiation; cell-cycle inhibitor; proliferative disorder; tissue degeneration; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIOVMAMGSARVAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cyclin dependent kinase - useful for gene other proliferative and differentiative
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Pred. No. 9.86e-84;
0; Mismatches 1; Indels
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W95096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beach D, Gyuris J, Lamphere L;
WPI; 97-393685/36.
N-PSDB; T74053.
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Best Local Similarity 99.4%;
Matches 154; Conservative
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23-JAN-1996; US-589981.
(MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric inhibitor of
therapy of cancer and
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WO9906540-A2
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DEPONENT MANAGER PARTE P
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Claim 63, Page 78-79; 88pp; English.

Claim 63, Page 78-79; 88pp; English.

Closs, particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (1) first gene construct transfection system (A) that comprises: (1) first gene construct comprising a sequence encoding an inhibition polypeptide containing at last one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (1) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (111) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic collycering the GCs to a cell for transfection. Also provided are nucleic polypeptide sequence (TCP) from an intranscellular protein that alters a cellular process when FP enters the cell, and (11) a transcellular collypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and a TCP. See X26220 for detailed uses of the recombinant transfection system. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers,
                                                                                                                                                                                                                             proteins including cyclin-dependent kinase
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Pred. No. 9.86e-84;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrosis and neurodegeneration
Claim 63; Page 86; 88pp; English.
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                                                                                                           Beach DH, Gyuris J, Lamphere L; WPI; 99-153770/13.
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Human p16p27 fusion protein.
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Matches 154; Conservative
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                                  US-902572.
                                                                                                                                                                                                                             Fusion and chimaeric
                                                                        (MITO-) MITOTIX INC.
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29-JUL-1997; US-9025
(MITO-) MITOTIX INC.
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                                                                                                                                                                                   N-PSDB; X26224
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29-JUL-1998;
29-JUL-1997;
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Transfection system (A) that comprises: (1) first gene construct comprising assertion system (A) that comprises: (1) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at least one CDK binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (11) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the GGs to a cell for transfection. Also provided are nucleic delivering the GGs to a cell for transfection. Also provided are nucleic polypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular consists of at least one CDK-binding motif and a TCP. See x26220 for detailed uses of the recombinant transfection system. The present
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Staim 63; Page 74-76; 88pp; English.

Claim 63; Page 74-76; 88pp; English.

The invention relates to novel inhibitors of cyclin-dependent kinases

CDKS), particularly CDK/cyclin complexes. It provides a recombinant

transfection system (A) that comprises: (i) first gene construct

comprising a sequence encoding an inhibitory polypeptide containing at

least one CDK-binding motif for binding and inhibiting activity of a CDK,

linked to a transcription regulator functional in eukaryotic cells; (ii)

second gene construct comprising a sequence encoding a polypeptide that

promotes endothelialisation, and (iii) a gene delivery composition for

delivering the GCs to a cell for transfection. Also provided are nucleic

collection and a construct of the complexity composition for conjecting a folypeptide sequence (TP) from an intracellular process when FP enters the cell, and (ii) a transcellular

cellular process when FP enters the cell, and (ii) a transcellular
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WESTANDES,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to novel inhibitors of cyclin-dependent kinases
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binding motif - used for regulation of cell proliferation and
differentiation, for treatment of, e.g. vascular injury, cancers,
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Pred. No. 9.86e-84;
0; Mismatches 1; Indels (
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W95095 standard; Protein; 380 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 98.18;
1 Similarity 99.48;
154; Conservative
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29-JUL-1998; U15759.
29-JUL-1997; US-902572.
(MITO-) MITORIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; X26223
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WO9906540-A2.
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polypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and a TCP. See X26220 for detailed uses of the recombinant transfection system. The present sequence represents a human p16(GS)p27 fusion protein.
                                                                                                                                                                       12 DPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVWMMGSARVAE 71
                                                                                                                                                                                                       61
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                                                                                                     Length 380;
                                                                                                   Score 1057; DB 1; Length 38(
Pred. No. 9.86e-84;
0; Mismatches 1; Indels
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Best Local Similarity 99.4%;
Matches 154; Conservative
                                                                  380 AA;
                                                                   Sequence
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Search completed: Thu Jul 20 08:34:54 2000 Job time : 9 secs.

Page 1

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	protein - protein database search, using Smith Thu Jul 20 08:36:50 2000; MasPar time 5. 401.877 Millic ut not generated. >US-09-016-869A-2 (1.156) from USO9016869A.pep	 19	cessing: Minimum Match 0% Listing first 45 summe	Database: a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1 Statistics: Mean 29.074; Variance 136.818; scale 0.212	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID Description Pred. No.	1 1078 100.0 156 4 PCT-US95-0 Sequence 2, Applicatio 4.93e-85 2 1078 100.0 156 3 US-08-30-5 Sequence 2, Applicatio 4.93e-85 4 1078 100.0 156 2 US-08-30-5 Sequence 2, Applicatio 4.93e-85 5 1078 100.0 156 2 US-08-89-5 Sequence 2, Applicatio 4.93e-85 6 1067 99.0 156 2 US-08-80-5 Sequence 2, Applicatio 4.93e-85 1078 100.0 156 2 US-08-80-5 Sequence 2, Applicatio 4.84e-84 1067 99.0 156 2 US-08-48-5 Sequence 2, Applicatio 4.84e-84 1067 99.0 156 2 US-08-48-5 Sequence 2, Applicatio 4.84e-84 10 1067 99.0 156 2 US-08-48-5 Sequence 2, Applicatio 4.84e-84 11 1067 99.0 156 2 US-08-50-5 Sequence 2, Applicatio 4.84e-84 12 1067 99.0 156 1 US-08-47-5 Sequence 2, Applicatio 4.84e-84 12 1067 99.0 156 1 US-08-50-5 Sequence 2, Applicatio 4.84e-84 12 1067 99.0 156 1 US-08-50-5 Sequence 2, Applicatio 4.84e-84 12 1067 99.0 156 1 US-08-50-5 Sequence 2, Applicatio 1.05e-80 156 1 US-08-50-5 Sequence 2, Applicatio 1.05e-80 156 1030 95.5 148 4 PCT-US96-0 Sequence 4, Applicatio 1.05e-80 15 1030 95.5 148 1 US-08-34-5 Sequence 12, Applicatio 1.05e-80 15 1030 95.5 148 1 US-08-34-5 Sequence 12, Applicatio 2.05e-54 17 1031 95.5 148 1 US-08-38-5 Sequence 8, Applicatio 2.05e-54 17 68-4 130 4 US-08-55-5 Sequence 8, Applicatio 2.05e-54 17 68-4 130 3 US-08-51-5 Sequence 8, Applicatio 2.05e-54 17 68-2 105 3 US-09-120-5 Sequence 14, Applicatio 2.05e-54 17 68-4 130 3 US-08-51-5 Sequence 14, Applicatio 2.05e-54 17 68-4 130 3 US-09-120-5 Sequence 14, Applicatio 2.05e-54 17 68-4 130 3 US-09-120-5 Sequence 14, Applicatio 2.05e-54 17 68-4 130 3 US-09-120-5 Sequence 14, Applicatio 2.05e-54 17 68-4 130 3 US-09-120-5 Sequence 14, Applicatio 2.05e-54 17 105-105-105-105-105-105-105-105-105-105-

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                                                                    Sequence 2, Application US/08581918A
Patent No. 6043030
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Beach, Manuel
APPLICANT: Hannon, Gragory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             156 AA
                                                                                                                                121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                  MEDIUM TREACHED FORM.

COMPUTER: FLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC COMPATIBLE
SOFTWARE: WordFad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-3NN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-3UN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 19-404
PRIOR APPLICATION DATA:
FILING DATE: 15-MAY-1994
PRIOR APPLICATION DATA:
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION DAT
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATTHEW P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08581918A
                                                                                                                                                                                                                           STANDARD;
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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US-08-581-918A-2
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Patent No. 5962316
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Benetrick, Douglas J.
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 11
CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIF: O2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                           Length 156;
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Pred. No. 4.93e-85;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMONIACATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE 156 AA; 16560 MW; 98948 CN;
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                                                                                                                                                                                                                                                                                      Match 100.0%;
Local Similarity 100.0%;
les 156; Conservative
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US-08-306-511A-2
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Sequence 2, Application US/08627610
Patent No. 591997
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Beach, Manuel
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCFFIELD
STREET: BOS State Street
CITY: Boston
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                    1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMMGSARVA 60
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                                                                                                                                                                                                                                                                   Score 1078; DB 2; Length 156;
Pred. No. 4.93e-85;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P
RECISTATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP6
TELECOMMUNICATION INFORMATION:
                                            NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 156 AA; 16560 MW; 98948 CN;
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Best Local Similarity 100.0%;
Matches 156; Conservative
                                                                                                                                                                                          amino acid
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ZIP: 02109
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                                                                             Score 1078; DB 2; Length 15 Pred. No. 4.93e-85; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
TITLE OF INVENTION: and Uses Related Thereto
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   156 AA
                                                                                                                                                                                                                                                                      121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                         CONTENT OF THE STATE OF STREET: ONE POST Office Square CITY: BOSTON CONDUTE: MACTON COMPUTER: THE PROPER: THE PROPER: THE PROPER: THE PROPER: THE PROPER: THE PROPER: THE PROPERTION COMPATIBLE OF SOFTWARE: ASCII(text) CURRENT APPLICATION NUMBER: US/08/893,274 FILING DATE: 15-7ULY-1997 CLASSIFICATION BODAR: APPLICATION NUMBER: US 08/248,812 FILING DATE: 14-SEPTEMBER-1994 PRIOR APPLICATION NUMBER: US 08/248,812 FILING DATE: 14-SEPTEMBER-1994 PRIOR APPLICATION NUMBER: US 08/227,371 FILING DATE: 14-APRIL-1994 PRIOR APPLICATION NUMBER: US 08/227,371 FILING DATE: 14-APRIL-1994 PRIOR APPLICATION NUMBER: US 08/154,915 FILING DATE: 18 NOVEMBER-1993 PRIOR APPLICATION NUMBER: US 07/991,997 FILING DATE: 17-DECEMBER-1992 PRIOR APPLICATION NUMBER: US 07/991,997 FILING DATE: 17-DECEMBER-1992
 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 156 AA; 16560 MW; 98948 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08893274 Patent No. 5968821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08893274
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                             Query Match
Best Local Similarity 100.0%;
Matches 156; Conservative
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US-08-893-274-2
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                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08480810

Patent No. 5801236
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSI GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Mashington
STATE: DC
                                                                                                            ó
                                                                                          Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 20005

ZUR: 20005

COMPUTER READALE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATE: US-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
                                                                                                           0; Indels
                                                                                                                                                                                                                                                          156 AA
                                                                                         Score 1078; DB 2;
Pred. No. 4.93e-85;
                                                                                                                                                                                                    121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                            121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                          PRT;
                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 156 AA; 16560 MW; 98948 CN;
                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08480810
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS:
                                      156 amino acids
                                                                                                                                                                                                                                                          STANDARD;
                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 156; Conservative
                                            amino acid
GY: linear
                                                                                                                                                                                                                                                        US-08-480-810-2
                                      LENGTH:
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Patent No. 5994095
GENERAL INFORMATION:
APPLICANT: Ramb, Alexander
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                               Score 1067; DB 1; Length 156;
Pred. No. 4.84e-84;
1; Mismatches 1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/251,938
FILING DATE: 01-UN-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
ENCE 156 AA, 16532 MW, 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                      NAME: Those, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2488.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08486047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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Local Similarity 98.7%;
nes 154; Conservative
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0; Gaps
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        SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORREY AGENT INFORMATION:
NAME: Inhen, Jeffrey.
REGISTRATION NUMBER: 28,957
REERRENCE/COCKET NUMBER: 28,957
REERRENCE/COCKET NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.0%; Score 1067; DB 2;
Best Local Similarity 98.7%; Pred. No. 4.84e-84;
Matches 154; Conservative 1; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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Patent No. 5739020
GENERAL INFORMATION:
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: MTSIE1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
PENCE 156 AA; 16532 MW; 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08487033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 antho acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-487-033-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Patent No. 5989815
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Canon-Albright, Lisa A.
APPLICANT: Canon-Albright, Lisa A.
TITLE OF INVENTION: GENELINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCE: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPOTER REDABLE FORM:
MEDIUM ITPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 202-962-4810
TELEPHAN: 202-962-8300
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acida
TYPE: amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1067; DB 2;
Pred. No. 4.84e-84;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 156 AA; 16532 MW; 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08848251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Best Local Similarity 98.7%;
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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Sequence 2, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Mamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
COUNTY: Washington
                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/508,735
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
APPLICATION NUMBER: PCT/US95/03316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24884-109348
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE 156 AA; 16532 MW; 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 24,957
REFERENCE/POCKET UNBER: 24,
TELECOMMUNICATION:
TELEPHONE: 202-962-4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202-962-8300
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Best Local Similarity 98.7%;
Matches 154; Conservative
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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US-09-120-130-2
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                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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E: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1067; DB 1; Length 156;
Pred. No. 4.84e-84;
1; Mismatches 1; Indels
                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                FILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
FRIOR APPLICATION DATA:
APPLICATION NOMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NOMBER: US 08/215,087
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
FRILNG DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLIANTIAN DAMER: 05
PRIOR APPLIANTIAN DAMER: 05
PRIOR APPLIANTION DATE: 18-MAR-1994
PRIOR APPLIANTION DATE: 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLIANTION DATE: 08/214,582
PRIOR APPLIANTION DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
RECEPHONE: 202-952-4810
                                                                                                                                                                                    APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-UNW-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE 156 AA; 16532 MW; 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.0%;
llarity 98.7%;
Conservative
                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 154; Conser
                                                         COUNTRY: US
ZIP: 20005
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-508-735-2
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Matches
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                                                                                                                        61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                     9
                                                                  Gaps
                                                    1 MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVA
                           ö
Score 1067; DB 2; Length 156;
Pred. No. 4.84e-84;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                          156 AA.
                                                                                                                                                             121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09120130
                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09120130
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Sequence 2, Application US/08508735

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61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1067; DB.1; Length 156;
Pred. No. 4.84e-84;
1; Mismatches 1; Indels 0; Gaps
                                                                                                                                         Sequence 2, Application US/08474177

Patent No. 5624819

GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Candon-Albright, Lisa A.
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY: UGA

ZIP: 20005

COUNTY: UGA

ZIP: 20005

COMPUTER READBABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHION DATA:

APPLICATION NUMBER: US/08/474,177

FILING DATE: 07-JUN-1995

CLASSIFCATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/251,938

FILING DATE: 17-WAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 18-WAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-WAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,369

FILING DATE: 18-WAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-WAR-1994

PRIOR APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-WAR-1994

PRIOR APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-WAR-1994

APPLICATION NUMBER: 28 08/214,582

FILING DATE: 18-WAR-1994

PRIOR APPLICATION NUMBER: 28 08/214,582

FILING DATE: 18-WAR-1994

ATCORNEY AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REERECOMMUNICATION INFORMATION:

TELEFORMONICATION INFORMATION:

TELEFORMATION:

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TOWAR
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MOLECULE TYPE: protein
ENCE 156 AA; 16532 MW; 98534 CN;
                                                                                                                  Sequence 2, Application US/08474177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202-962-8300
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Best Local Similarity 98.7%;
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels 0;
Patent No. 6037462
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: WTG1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 156;
                                                                                                                                                                                                    STATE: DC
COUTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,130
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 08/251,938
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTONEY/AGENT INFORMATION:
NAME: Then, Jeffrey L.
REGISTRATION NUMBER: 28,957
RESERENCE/DOCKET NUMBER: 28,957
RESERENCE/DOCKET NUMBER: 28,957
RESERENCE/DOCKET NUMBER: 28,957
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1067; DB 3;
Pred. No. 4.84e-84;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
FENCE 156 AA; 16532 MW; 98534 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 156 anino acids
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Best Local Similarity 98.7%;
Matches 154; Conservative
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121 ELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 157
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PCT-US93-09945-4
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61 ELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05252
FILING DATE: Not yet assigned
CLASSIFICATION:
                                                                                                                                                      Sequence 5, Application PC/TUS9605252
GENERAL INFORMATION:
APPLICANT:
TILLE OF INVENTION: p19: A Cell Cycle Inhibitor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
                                                                                    Ź
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Weber, Ellen L. REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 02307B-059910PC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1067; DB 4;
Pred. No. 4.84e-84;
0; Mismatches 0
                                                                                    157
                                    121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..157
OTHER INFORMATION: /note= "human, p16"
ICE 157 AA; 16674 MW; 100395 CN;
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,093
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                    PRT;
                                                                                                                                          Sequence 5, Application PC/TUS9605252
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 157 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.4%;
Matches 156; Conservative
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PCT-US96-05252-5
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236 MORAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIOVMMMGSARVA 295
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                                                                                                                                                                                                                                                                  Sequence 2, Application US/08589981
Patent No. 5672508
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GYULIS, Jeno
APPLICANT: Lampher, Lou
APPLICANT: Baach, David H.
TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 4
CORRESSEDE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
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                                                                                                        391 AA.
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98.7%; Pred. No. 9.03e-84;
vative 1; Mismatches 1;
120 ELGHRDVARYLRAAAGGIRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICALLO...
FILING DATE.
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-069
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
IELEPHONE: (617) 227-5941
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acids
TYPE: ... 1*near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
FENCE 391 AA; 42306 MW; 652242 CN;
                                                                                                        PRT;
                                                                                                                                                                                                                                 Sequence 2, Application US/08589981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                      STANDARD;
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ses 154; Conservative
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1RY: USA
02109
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US-08-589-981-2
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COUNTRY:
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TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SOUGHCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 41sk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1030; DB 4; Length 148;
Pred. No. 1.05e-80;
0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                            FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 148 AA; 15844 MW; 88737 CN;
                                                                                       Sequence 4, Application PC/TUS9309945
GENERAL INFORMATION:
APPLICANT:
                                                                 Sequence 4, Application PC/TUS9309945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 148; Conservative
               XXXXX
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61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120 69 EPNCADPALLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128 å ò 셤

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:35:12 2000; MasPar time 11.77 Seconds 625.481 Million cell updates/sec Run on:

Tabular output not generated.

Description: Perfect Score:

>US-09-016-869A-2 (1-116) from US09016869A.pep 1078 1 MDPAAGSSMEPSADWLATAA......TRGSNHARIDAAEGPSDIPD 156 Sequence:

PAM 150 Gap 11 Scoring table:

142080 seqs, 47172406 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 43.845; Variance 94.938; scale 0.462 pir63 1:pirl 2:pir2 3:pir3 4:pir4 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	3.86e-175	1.59e-110	9.09e-110	4.46e-98	3.82e-41	5.04e-39	1.70e-38	7.29e-32	1.75e-30	4.14e-29	3.58e-12	4.30e-11	4.30e-11	4.30e-11	6.11e-11	_	_	5.64e-09	5.64e-09	5.64e-09	5.64e-09	5.64e-09	8.61e-08
Description	cyclin dependent kina	plsink4b - mouse	P	p16INK4a - mouse	cyclin-dependent kina	CDK4/CDK6 1phibitor p	cyclin-dependent kina	CDK6 inhibitor p18 -	CDK4/CDK6 inhibitor p	SINK	ankyrin 2, neuronal l	ì	ij	1,	er er	- mouse	ankyrin 3, long splic	-related	ankyrin-related unc-4	elegans ankyrin-relat	ankyrin-related unc-4		ankyrin - fruit fly (
A	JE0141	I78845	B55479	158352	A57378	A57379	B57378	A55479	B57379	I52720	S37431	B35049	A35049	SJHUK	537771	I49502	A55575	A57282	T15345	T15346	T15344	T15347	T13940
DB	7	~	~	N	~	~	~	N	~	~	~	~	7	Н	7	N	N	~	~	~	~	~	7
% Query Match Length	156	130	138	167	164	166	166	168	168	41	3924	1856	1880	1881	1848	1862	4377	1786	1809	1815	1867	2039	1549
& Query Match	99.0	67.6	67.3	61.5	32.7	31.6	31.4	27.8	27.1	26.3	16.8	16.1	16.1	16.1	16.0	16.0	15.3	14.8	14.8	14.8	•	•	14.1
Score	1067	729	725	663	353	341	338	300	292	284	181	174	174	174	173	173	165	160	160	160	160	160	152
Result No.	-	7	٣	4	ស	Q	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

#authors Say359 356:704-707
#authors Serrano, M.; Hannon, G.J.; Beach, D.
#journal Nature (1993) 366:704-707
#title A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D/CDK4.
#cross-references MJD:94081956
#accession S39359

REFERENCE #authors #journal #title

IS9S85

Kamb, A.; Gruls, N.A.; Weaver-Feldhaus, J.; Liu, O.;

Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.;

Johnson, B.E.; Skolnick, M.H.

Science (1994) 264:436-440

#authors

REFERENCE

#journal

##status ##molecule_type mRNA ##residues 9-34,'V',36-156 ##label SER ##note this sequence has been corrected in reference I59268

	6 ##label HUA e Hella cell A.; Demetrick, D.J.; Spillare ', S.P.; Bennett, W.P.; Forres ', M.; Beach, D.H. and altered expression of pl 95062202 slation not shown; translated 2 ##label RES B:S74232; NID:9710467 report is a correction
40664 2 2 4142 2 323 2 3 23 2 3 2 3 2 3 2 3 2 3 2 3	# E + N X EO 4 # N 0
3.2 1964 2.6 323 2.2 20 3.2 323 2.2 20 3.2 323 1.1.6 2331 1.1.4 2437 1.1.4 2437 1.1.4 2437 1.1.4 2437 1.1.4 2437 1.1.6 679 1.1.6 679 1.1.0 679 1.1	15 Charles Control 15
33.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 11.6 2.2 11.4 2.2 11.4 2.2 11.4 2.2 11.4 2.2 11.4 2.2 11.4 2.2 11.4 2.2 11.4 2.2 11.4 2.2 2.2 3.3 3.3 3.3 3.3 3.3 3.3 3.3 3.3	tal_sou Dks9z66 Oks9z666 Dkssz Broc. b Mutatics MI 159268 Ctype Di Ctype Di
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24 142 25 141 26 138 27 136 28 132 29 132 30 128 31 125 34 123 34 123 35 123 36 123 36 123 37 123 38 123 39 119 40 111 42 118 44 111 ENTRY 45 118 ACCESSIONS REFERENCE ##molecular ##molec	REFERENCE PROBLEM PROB

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Chinese J. Biotechnol. (1997) 13:105-107
Molecular cloning and sequencing of P16 ink4 cDNA from hela
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C.; Beach, D.; Sherr,
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                                                                                       translation not shown; translated from GB/EMBL/DDBJ
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pl5INK4b - mouse
#formal_name Mus sp. #common_name mouse
02.Aug-1996 #sequence_revision 02-Aug-1996 #text_change
28.Feb-1997
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#title A cell cycle regulator potentially involved in genesis many tumor types.
#cross-references MUID:94204645
#accession I59585
                                                                                                                                                                                                                                                                               p151NK4b
#length 130 #molecular-weight 13788 #checksum 7879
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##cross-references GDB:335362; GDB:CDKN2A; OMIM:600160
#map_position 9p21.9p21
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins
KEYWORDS cell cycle control; protein kinase inhibitor; tumor suppressor
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Best Local Similarity 98.7%; Pred. No. 3.86e-175;
Matches 154; Conservative 1; Mismatches 1;
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Pred. No. 1.59e-110;
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Trono, D.; Richter, K.H.; Walker,
C.J.; Serrano, M.
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                                                                                                                                            ##cross-references GB:S69804; NID:g546272
                                                                                                                         51-152 ##label RE2
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Matches 106; Conservation
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##residues 51-1
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B55479 #type complete
CDK4 inhibitor pl4(INK4B/MTS2) - human
CDK6-associated protein pl5(INK4B); cyclin-dependent kinase
inhibitor 2B; multiple tumor suppressor 2
#formal_name Homo sapiens #common_name man
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hannon, G.J.; Beach, D.
Nature (1994) 371:257-261
p15(INK4B) 1s a potential effector of TGF-beta-induced cell
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PERENCE 152713
#authors Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.;
Papadopoulos, N.; Markowitz, S.; Willson, J.K.; Kinzler, K.W.; Vogelstein, B.

#journal Cancer Res. (1994) 54:6353-6358
#title Deletion of p16 and p15 genes in brain tumors.
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                                                                                                 #authors Guan, R.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.; Xiong, Y. Genes Dev. (1994) 8:2939-2952 #title Growth suppression by pl8, a pi6(INK4/MTS1)- and pl4 (INK4/MTS1)-related CDK6 inhibitor, correlates with wild-type pRb function.
                                                                      70 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAWGRLPVDLAEEQGHRDIARYLHAATG 129
16 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.;
Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III,
Johnson, B.E.; Skolnick, M.H.
Science (1994) 264:436-440
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#length 138 #molecular-weight 14722 #checksum 1236
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#map_position 9p21-9p21
FWORDS cell cycle control; protein kinase inhibitor; tumor
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##residues 1-138 ##label GUA
##cross-references GB:U17075; NID:g639715; PID:g639716
##experimental_source HeLa cells
SNCE 847593
                                                                                                                                                                                                                                                                                                                                                            28-May-1999
B55479; S47593; I81183; I52713
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#ecross-references GB:S75756; NID:g861470
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##residues 53-138 ##label KAM
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1-166 ##label CHA
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##residues 1-16
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     #map_position 19p13
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Identification of human and mouse pl9, a novel CDK4 and CDK6
inhibitor with homology to pl6(ink4).
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Cloning and characterization of murine p16INK4a and p15INK4b
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C.; Beach, D.; Sherr,
                                                                                                                                                                                                                                                69 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
                                                                                                                                                                                                                   78 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYLRTATG 137
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                                                                                                                                          1 MESAADRLARAA-QGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHVAALLLNYGA 59
                                                                                                           18 LASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMMGSARVAELLLLHGAEPNCADP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyclin-dependent kinase inhibitor p19 - human #formal_name Homo sapiens #common_name man 08-reb-1996 #sequence_revision 08-reb-1996 #text_change 22-Jun-1999 A57378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p161NK4a
#length 167 #molecular-weight 17870 #checksum 1257
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ### preliminary; translated from GB/EMBL/DDBJ ##molecule_type mRNA | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 1-167 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010 | 2010
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Length 138;
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Pred. No. 4.46e-98;
20; Mismatches 14; Indels
                                                     Indels
Score 725; DB 2; L. Pred. No. 9.09e-110; 6; Mismatches 9;
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Trono, D.; Richter, K.H.; Walker,
C.J.; Serrano, M.
                                                                                                                                                                                                                                                                                                                                                                               IS8352 #type complete
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#accession I58352
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Query Match 67.3%;
Best Local Similarity 87.5%;
Matches 105; Conservative
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Local Similarity 72.2%;
hes 91; Conservative
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##molecule_type_mRNA
#fresidues 1-166 ##label HIR
##residues 6B:U1959; NID:9790568; PIDN:AAC52194.1; PID:9790569
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
KEYWORDS cell cycle control
SUMMARY #length 166 #molecular-weight 17894 #checksum 3512
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Identification of human and mouse pi9, a novel CDK4 and CDK6 inhibitor with homology to pi6(ink4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. (1995) 15:2672-2681
Novel INK4 proteins, p19 and p18, are specific inhibitors of
the cyclin D-dependent kinases CDK4 and CDK6.
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                                                                                                                                                                                                                                                                                                                                  71 TSG-TSPVHDAARTGFLDTLKVLVEHGADVNVPDGTGALPIHLAVQEGHTAVVSFLAAES 129
                                                                                                                                                                                                                                                                                                                                                            *superfamily unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology #length 164 #molecular-weight 17352 #checksum 5271
                                                                                                                                                                                                                      11 LSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSTAIALELLKQGASPNVQD 70
                                                                                                                                                                                                                                                     69 VQDASG-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFL 126
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cyclin-dependent kinase inhibitor p19 - mouse
cyclin-dependent kinase inhibitor p19 - mouse
#formal_name Mus musculus #common_name house mouse
08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
20-Sep-1999
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Pred. No. 5.04e-39;
19; Mismatches 39; Indels
                                                                                                         Score 353; DB 2; Length 164
Pred. No. 3.82e-41;
19; Mismatches 39; Indels
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#accession B57378
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                                                                                                         Query Match 32.7%;
Best Local Similarity 50.0%;
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Local Similarity 49.6%;
les 59; Conservative
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A57379
                                                                                                                                                                  60; Conservative
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Gaps

Length 168;

SUMMARY

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##status preliminary
##molecule_type mRNA
##residues
# = 1.66 ##label HIR
##csos-references GB:U19596; NID:g790566; PIDN:AAC52193.1; PID:g790567
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
KEYWORDS cell cycle control
#length 168 #molecular-weight 18066 #checksum 8831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L. Cancer Res. (1995) 55:1607-1612
Association of rat pl51NK4B/pl61NK4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal
                                                                 Mol. Cell. Biol. (1995) 15:2672-2681
Novel INK4 proteins, p19 and p18, are specific inhibitors of
the cyclin D-dependent kinases CDK4 and CDK6.
noes MolD:95257948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 PNLKDGTGFA-VIHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKEGHLPVVFF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLERGAN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152720 #type fragment
gene pl51NK4B protein - rat (fragment)
#formal_name Rattus sp. #common_name rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
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                           Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun,
                                                                                                                                                                                                                                                                                                                                                                                     Score 292; DB 2; Length 168
Pred. No. 1.75e-30;
29; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 MAMGSARVAELLLIHGAEPNCADPATLTRPVHDAAREGFLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAMGSAQVAELLLIHGAEPNCADPATLTRPVHDAAREGFLD 41
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Pred. No. 4.14e-29;
1; Mismatches 0
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##cross-references GB:S77734; NID:g998711
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#length 41 #checksum 3296
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#accession I52720
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Best Local Similarity 43.0%;
Matches 52; Conservative
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Best Local Similarity 97.6%;
Matches 40; Conservative
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##residues 1-41
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CDK6 inhibitor p18 - human
Cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent
Kinase CDK6 inhibitor p18
#formal_name Homo sapiens #common_name man
23.Mar-1995 #sequence_revision 23-Mar-1995 #text_change
##Cross-references GB:U20497; NID:q791204; PIDN:AAA85437.1; PID:q791205
FICATION #superfamily unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

#length 166 #molecular-weight 17920 #checksum 3767
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##residues 1-168 ##label GUA
##cross-references GB:U17074; NID:g639713; PIDN:AAC50074.1; PID:g639714
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O'Keefe, C.L.; Matera, A.G.; Xiong, Y.
Genes Dev. (1994) 8:2939-2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #gene ##ferross-references GDB:594931
#map_position lp32-1p32
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
KEYWORDS cell cycle control; protein kinase inhibitor; tumor
                                                                                                                                                                                                                               3 EPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVWRLGNPEIARRLLLRGAN 62
                                                                                                                                                                                                          GDRLSGARPRGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPN 68
                                                                                                                                                                                                                                                                                              69 VQDASG-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFL 126
                                                                                                                                                                                                                                                                                                                      10 EPSADWILATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLILLHGAE 69
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                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #fitle Growth suppression by p18, a p16(INK4/MTS1)- and p14 (INK4/MTS4B/MTS2)-related CDK6 inhibitor, correlates with wild-type pRb function. #cross-references MUID:95095079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          suppressor
#length 168 #molecular-weight 18127 #checksum 9379
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                                                                                                                    Length 166;
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                                                                                                               Score 338; DB 2; Length 166
Pred. No. 1.70e-38;
20; Mismatches 39; Indels
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35; Mismatches 48; Indels
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                                                                                                           Iocal Similarity 48.7%;
es 58; Conservation
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Best Local Similarity 39.6%;
Matches 55; Conservative
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Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.;
Speicher, D.; Cheung, M.C.; Ran, Y.W.; Palek, J.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
CDNA sequence for human erythrocyte ankyrin.
                                                                                                                                                                                                                                                                                                                                                                          20 AAR-GRVEEVRALLEAVALPNAPNSYGRRPIQVM-MMGSARVAELLLLHGAEPNCADPAT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B35049 #type complete
ankyrin 1, erythrocyte splice form 3 - human
ankyrin 2.1, erythrocyte; ankyrin-R
ankyrin 2.2, erythrocyte
#formal_name Homo sapiens #common_name man
17.Nov-1995 #sequence_revision 17.Nov-1995 #text_change
10.Jul-1998
                                                                                                                                                                                                                                          #molecular-weight 430340 #checksum 3664
thomology *label AN11\
thomology *label AN12\
thomology *label AN13\
thomology *label AN14\
thomology *label AN15\
thomology *label AN15\
thomology *label AN17\
thomology *label AN17\
thomology *label AN11\
thomology *label AN20\
thomology *label AN20\
thomology *label AN21\
                                                                                                                                                                                                                                                                               DB 2; Length 3924;
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Pred. No. 3.58e-12;
20; Mismatches 53; Indels
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#map_position 8pl1.2 * 8pl1.2
CLASSIFICATION alternative splicing ankyrin repeat homology
REYWORDS alternative splicing
                                                     #domain ankyrin repeat he #domain ankyrin repeat he
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#domain ankyrin repeat
#length 3924 #molecular-well
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Best Local Similarity 38.1%;
Matches 48; Conservative
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domain
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##residues 1-189
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628-660
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727-759
760-792
793-825
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REFERENCE
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238-270
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2-1856
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J. Gall Biol. (1993) 123:1463-1473
440.kD ankyrinB: structure of the major developmentally
regulated domain and selective localization in unmyelinated
                                                                                                                                                                                                                                       #authors Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
#Journal J. Cell Biol. (1991) 114:241-253
#title Isolation and characterization of cDNAs encoding human brain ankyrins reveal a family of alternatively spliced genes.
#cross_references_MUID:91302466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
##residues 463-474,'PE',477-495 ##label TSE
##cross-references GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
:NCE A49462
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*product ankyrin 2, short form *status predicted *label MA2\
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   06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                      S37431; A39643; B39643; A40334; A49462; S14533; S14569
                                                                        Chan, W.
submitted to the EMBL Data Library, September 1993
S37431
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                                                                                                                                                              ##residues 1-3924 ##label CHA
##cross-references EMBL:226634; NID:9406287; PIDN:CAA81387.1;
PID:9406288
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##cross-references EMBL:X56958
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##Cross-references GDB:127607; OMIM:106410
#map_position 4q25-4q27
CLASSIFICATION #superfam*1**
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##residues 1-2077 ##label OT1
##cross-references GB:X56957
cession B39643
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##residues
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                     13-Aug-1999
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232-264
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                                    ACCESSIONS
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#label MAT\
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Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
CDNA sequence for human erythrocyte ankyrin.
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#label MA2\
                                                                                                                                                                                                                                                                                                                                                                      16 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMM-GSARVAELLLLHGAEPNCAD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A35049 #type complete
ankyrin 1, erythrocyte splice form 2 - human
ankyrin 2.1, erythrocyte; ankyrin-R
ankyrin 2.2, erythrocyte
#formal_name Homo sapiens #common_name man
27.401-1990 #sequence_revision 01-Oct-1992 #text_change
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               567 KNGLT-PLHVAVHHNNLDIVKLLLPRGGSP-HSP-AWNGYTPLHIAAKQNQVEVARSL 621
                                                                                                                                                                                                                         #molecular-weight 203445 #checksum 6521
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#domain ankyrin repeat homology #label ANI
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#feross-references GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
REYWORDS alternative splicing; cytoskeleton
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16; Mismatches 50; Indels
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*#molecule_type mRNA
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Best Local Similarity 39.0%;
Matches 46; Conservative
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568-600
601-633
634-666
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77-109
110-142
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205-237
238-270
271-303
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#authors Hermann, J.; Barel, M.; Frade, R.
#journal Blochem. Britial component of complement.
#cross-references MIDI:95071348
#accession PG2220
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##residues 2-7,'X', 9-17,'X',19-20,'T',22-30;733-749,'A',751-753;

#828.833,'X',835-855,'X',857-862,'XX',862-871,

1106-1120,'XX',1123-1128;1149-1172;1282-1285,'E',

1287-1288;1307-1332;1345-1365,'X',1367;1383-1427;

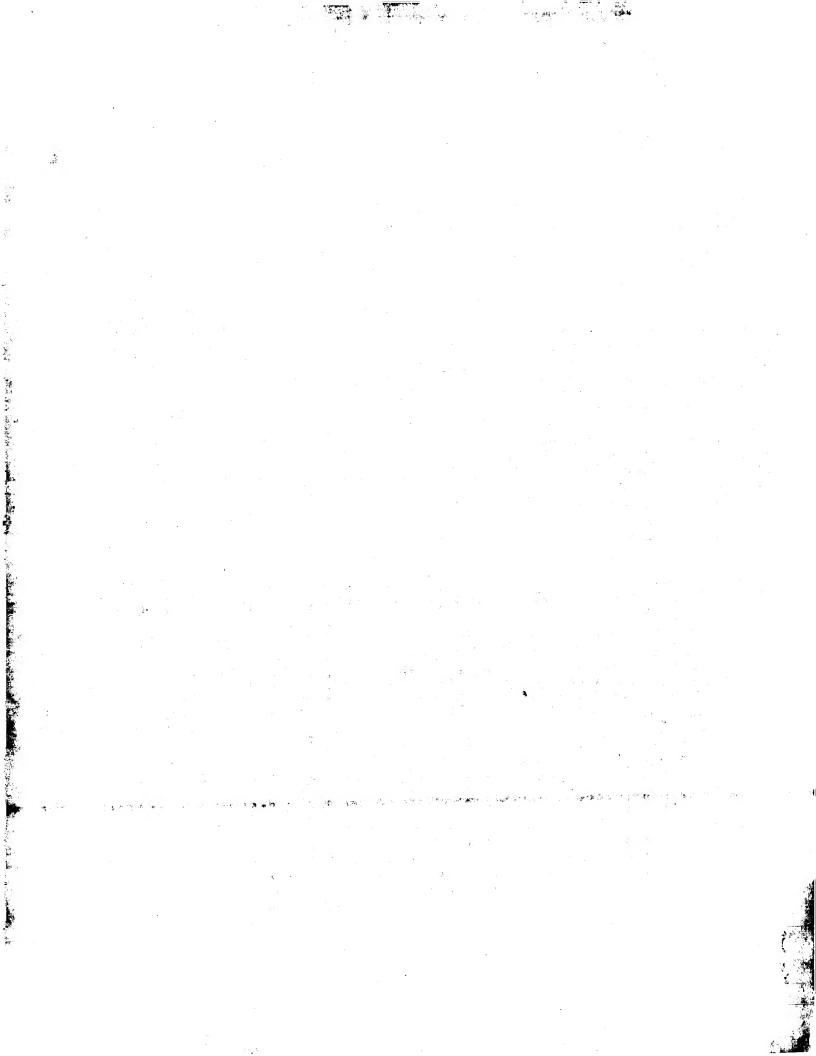
##note 845-Arg and 1392-Thr were also found
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##molecule_type mRNA
##molecule_type mRNA
##residues 1-1881 ##label LUI
##cross-references EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702
##ncession A33219
##ncession A33219
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#journal Nature (1990) 344:36-42
#title Analysis of CDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle control proteins.
#cross-references MUID:90158830
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#journal J. Biol. Chem. (1990) 265:10589-10596
#title Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger and spectrin.
#cross-references MUID:90285190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              #formal_name Homo sapiens #common_name man
30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
22-0un-1999
S08275; A33219; PC2220; A35443
S08275
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#domain ankyrin repeat homology #label AN17\
#domain ankyrin repeat homology #label AN18\
#domain ankyrin repeat homology #label AN18\
#domain ankyrin repeat homology #label AN2\
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#domain ankyrin repeat homology #label AN2\
#domain ankyrin repeat homology #label AN21\
#domain ankyrin repeat homology #label AN21\
#domain ankyrin repeat homology #label AN3
#length 1880 #molecular-weight 20606 #checksum 6968
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                                                                                                                                                                                                                                                                                                        Score 174;
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##residues 910-929 ##label HER
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Best Local Similarity 39.0%;
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176-208
209-241
242-274
275-307
308-340
341-373
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737-769
770-802
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638-670
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Lux, S.E.; Barker, J.E.
J. Biol. Chem. (1993) 268:9533-9540
Complex patterns of sequence variation and multiple 5' and 3'
ends are found among transcripts of the erythroid ankyrin
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#product ankyrin 2.2, erythrocyte #status predicted
#label MAT2\
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ankyrin, erythrocyte - mouse
#formal_name Mus musculus #common_name house mouse
27-May-1994 #sequence_revision 03-Aug-1995 #text_change
13-Aug-1999
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                                                                                                                                                                                                                           #region anion exchange protein binding domain ankyrin repeat homology #label ANO1, #domain ankyrin repeat homology #label ANO2, #domain ankyrin repeat homology #label ANO3, #domain ankyrin repeat homology #label ANO3, #domain ankyrin repeat homology #label ANO5, #domain ankyrin repeat homology #label ANO5, #domain ankyrin repeat homology #label ANO6, #domain ankyrin repeat homology #label ANO9, #domain ankyrin repeat homology #label ANO9, #domain ankyrin repeat homology #label ANO9, #domain ankyrin repeat homology #label ANIO, #domain ankyrin repeat homology #label ANII, #domain ankyrin repeat homology #label ANII)
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Pred. No. 4.30e-11;
16; Mismatches 50; Indels 6;
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##cross-references EMBL:X69063; NID:9311816; PIDN:CAA48801.1;
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#gene
#fcross-references GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #puperfamily ankyrin; ankyrin repeat homology
KEYWORDS alternative splicing; phosphoprotein
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#accession S37771
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Matches 46; Conservative
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Pred. No. 6.11e-11;
17; Mismatches 50; Indels 6;
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AN08\
AN09\
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PID:g311817
#superfamily ankyrin; ankyrin repeat homology
alternative splicing
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Best Local Similarity 38.1%;
Matches 45; Conservative
            CLASSIFICATION
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Search completed: Thu Jul 20 08:35:26 2000 Job time : 14 secs.



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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch pp

Thu Jul 20 08:35:43 2000; MasPar time 7.46 Seconds 637.235 Million cell updates/sec Tabular output not generated. Run on:

>US-09-016-869A-2 (1-156) from US09016869A.pep 1078 1 MDPAAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

83857 segs, 30454973 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot38 1:swissprot Database:

Mean 44.859; Variance 85.215; scale 0.526 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.98e-	AS 6.89e-126	AS 5.00e-125	'n	AS 9.94e-112	AS 5.27e-93	AS 3.10e-49	AS 1.29e-44	AS 1.72e-36	AS 6.33e-35	NT 3.37e-14	NT 3.37e-14	2. 5.58e-13	8.30e-13	СН 8.65е-08	TE 1.81e-07		Н	44		H H 4 8	HH 4 8 H	HH 4 8 HH
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GABD_MOUSE	GLS1_CAEEL	RNSA_MOUSE	NTC1_MOUSE	PHLB_SERLI	GABC_MOUSE	GABB_MOUSE	SKD3_MOUSE	GABC_HUMAN	GABB_HUMAN	LATA_LATMA	FNRL_RHOSH	YZ82_MYCTU	YB13_FOWPM	YOAB_ECOLI	YEO7_MYCTU	YIL2_YEAST	BCL3_HUMAN	EGIN_MOUSE	UL17_HSV11	Y050_HUMAN	ORP1_HUMAN
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ALIGNMENTS

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CDMZ_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 36, Last sequence update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKXZA OR CDKXZ. HOMO SAPIENS (Human). EUKARYOta: Wetazoa: (Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A. MEDLINE; 94081956. Serrano M., Hannon G.J., Beach D.; A new requistcry moiff in cell-cycle control causing speinhibition of cyclin D/CDK4."; Nature 366:704-707(1993). [2] SEQUENCE OF 51-152 FROM N.A. MEDLINE; 94204645.	CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last sequence update) 15-UUL-1999 (Rel. 38, Last sequence update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUNOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO SUPPRESSOR 1) (MTS1). EUKARYOUTS (CONTAGATA; Cranlata; Vertebrata; Mamma EUKARYOUT; Primates; Catarrhini; Hominidae; Homo. EUKARYOUTS FROM N.A. MEDLINE; 94081956. Serrano M., Hannon G.J., Beach D.; Amen regulatory motif in cell-cycle control causing speinhibition of cyclin D/CDK4.; Nature 366:704-707(1993). [2] SEQUENCE OF 51-152 FROM N.A. MEDLINE; 94204645.	SULT 1 PA1771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-JUL-1998 (Rel. 36, Last sequence update) 17-JUL-1998 (Rel. 36, Last sequence update) 18-JUL-1998 (Rel. 36, Last sequence update) 19-JUL-1998 (Rel. 36, Last sequence update) 19-JUL-199
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CDM2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE THOR SUPPRESSOR 1) (MTS1). HOMO SADIORS (Human). EUKARYOta; Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A. MEDLINE; 94081956.	CDN2_HUMAN STANDARD; PRT; 156 AA. CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO suptens (Human). Eukaryota; Metazoa (Chordata; Cranlata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo. ELSE PROM N.A. MEDLINE; 94081956.	SULT 1 PAT71: 015191; 01-NOV-1995 (Rel. 32, Created) 15-UL-1998 (Rel. 34, Last sequence update) 15-UL-1999 (Rel. 36, Last sequence update) 15-UL-1999 (Rel. 38, Last annotation update) 15-UL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (MULTIPLE TUWOR SUPPRESSOR 1) (MTS1). CDKNAS OR CDKN2. Homo sapiens (Human). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A. MEDLINE; 94081956.
CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUNOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO saptens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Pilmates; Catarrhini, Hominidae; Homo. SEQUENCE FROM N.A. MEDLINE; 94081956.	CDN2_HUMAN STANDARD; PRT; 156 AA. CDN2_HUMAN (15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 36, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 36, Last annotation update) 15-JUL-1999 (Rel. 36, Last annotation update) 15-JUL-1999 (Rel. 36, Last annotation update) COKNIA OR CDKN12. HUMBILIDE TUNKA) EURAPORT (HUMAN). EURAPORT (HUMAN). EURAPORT (HUMAN). EURAPORT (HUMAN). SEQUENCE FROM N.A. MEDILINE: 94081956.	SULT 1 CDNHUMAN CDNHUMAN P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1998 (Rel. 36, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMON SUPPRESSOR 1) (MTS1). CDKX2A OR CDKX3. HOMO Sapiens (Human). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; P1mates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A. MEDLINE: 94081956.
CDM2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-WOV-1995 (Rel. 32, Created) 15-UL-1998 (Rel. 36, Last sequence update) 15-UL-1999 (Rel. 36, Last sequence update) 15-UL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUWOR SUPPRESSOR 1) (MTS1). CDKRAR OR CDKNA. HOMO SAPPIENS (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A.	CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKXAA OR CDKXA. HOMO Sapiens (Human). Eukaryota: Metazoa; Chordata; Craniata: Vertebrata: Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A.	SULT 1 CON2_HUAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last sequence update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CMULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO SAPLENS (Human). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mamma Butheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A.
CDM2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). HOMO SAPIENS (HUMAN). EUKARYOTA: MECAZOA: Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A.	CDN2_HUMAN STANDARD; PRT; 156 AA. CDN2_HUMAN STANDARD; PRT; 156 AA. 01-NOV-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). HOMO SADIENS (Human). EUKARYOTA: Wetazoa: Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A.	SULT 1 CDN2_HUAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKNZA OR CDKN2. HOMO sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A.
CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01.NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUNOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO saptens (Human). Eukaryota: Metazoa; Chordata; Craniata: Vertebrata: Mamma Eutheria: Primates; Catarrhini; Hominidae; Homo.	CDN2_HUMAN STANDARD; PRT; 156 AA. CDN2_HUMAN (15191; 01-NOV-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 36, Last annotation update) 15-UUL-1999 (Rel. 38, Last annotation update) 15-UUL-1999 (Rel. 38, Last annotation update) 15-UUL-1999 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 36, Last annotation update) 15-UUL-1998 (Rel. 36, Last annotation update) COKILIPLE TUNOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO Saplens (Human). Eukaryotts, Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo.	SULT 1 CDN2_HUMAN STANDARD; PRT; 156 AA. CDN2_HUMAN P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMON SUPPRESSOR 1) (MTS1). CDKAZA OR CDKN3. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutharyota; Primates; Catarrhini; Hominidae; Homo.
CDNZ_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 015191; 015191; 015191; 015192; 01-NOV-1995 (Rel. 32, Created) 15-UUL-1999 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKNAA, OR CDKNA. Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo.	CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKXAA OR CDKXA. Homo sapiens (Human). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo.	CDN2_HUAN STANDARD; PRT; 156 AA. CDN2_HUAN STANDARD; PA1771; (15191; 01.NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last senociation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) CDKN2A OR CDKN2. HOMO SUPPRESSOR 1) (MTS1). HOMO Suplens (Human). ELKETYOCE: Metazoa; Chordata; Cranlata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo.
CDM2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). HOMO sapiens (Human). EUKARYOta: Mecazoa; Chordata; Craniata; Vertebrata; Mamma Eukheria; Primates; Catarrhini; Hominidae; Homo.	CDN2_HUMAN STANDARD; PRT; 156 AA. CDN2_HUMAN STANDARD; PRT; 156 AA. 01-NOV-1995 (Rel. 32, Created) 15-UUL-1999 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDNX2A OR CDKN2. Homo sapiens (Human). Eukaryota; wetazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo.	SULT 1 CON2_HUAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-UL-1998 (Rel. 36, Last sequence update) 15-UL-1999 (Rel. 38, Last annotation update) 15-UL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUWOR SUPPRESSOR 1) (MTS1). CDKNAR OR CDKN2. Homo sapiens (Human). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhin1; Hominidae; Homo.
CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO saptens (Human). Elkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo.	CDN2_HUMAN STANDARD; PRT; 156 AA. CDN2_HUMAN (15191; 015191; 015191; 015191; 015191; 015192; 01-NOV-1995 (Rel. 32, Created) 15-UUL-1999 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUNOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO saptens (Human). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mamma Butheria; Primates; Catarrhini; Hominidae; Homo.	SULT 1 CDN2_HUAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKNZA OR CDKNZ. Homo sapiens (Human). Eukaryota: Metazoa: Chordata; Cranlata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo.
CDNZ_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) 15-UUL-1999 (Rel. 38, Last annotation update) 15-UUL-1999 (Rel. 38, Last annotation COKAL) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKARA OR CDKNA. HOMO saplens (Human). Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma Entheria: Primates: Cararrhin; Hominiae. Homo	CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKX2A OR CDKX3. HOMO Sapiens (Human). Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma Entheria: Primates: Cararrhin; Hominiae. Homo	SULT 1 CDN2_HDAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 36, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN3. HOMO Sapiens (Human). ENKAYPOGE; Medezoa; Chordata; Cranlata; Vertebrata; Mamma Butharia: Primates: Catarrhia: Primates: Catarrhia: Homo Homo
CDM2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). HOMO sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma	CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOY-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CMULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. HOMO Saptens (Human). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mamma	SULT 1 CDN2_HUAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-UL-1998 (Rel. 36, Last sequence update) 15-UL-1999 (Rel. 38, Last sequence update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKNZA OR CDKNZ. HOMO Saplens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma
CDM2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. Homo sapiens (Human). Eukaryota: Metazoa; Chordata; Cranlata; Warmma	CDN2_HUMAN STANDARD; PRT; 156 AA. CDN2_HUMAN STANDARD; PRT; 156 AA. 10-100V-1995 (Rel. 32, Created) 15-UUL-1999 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last snonctation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKN2A OR CDKN2. Homo saptens (Human). ELKARTVOR: Metazoa; Chordata; Cranlata; Wartebrata; Mamma	SULT 1 CDN2_HUAN STANDARD; PRT; 156 AA. P42771; (15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). FORMARA OR CDKW2. HOMO Sapiens (Human). EMARYOCE: Metazoa; Chordata; Cranlata; Mamma
CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update) 15-UUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTPLE TUNNS SUPPRESSOR 1) (MTS1). CDKNZA OR CDKNZ. HOMO Saplens (Human).	CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKAZA OR CDKAZ. HOMO Saplens (Human).	SULT 1 DATE 10 STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 36, Last annotation update) 15-UUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CMULTIPLE TUMOR SUPPRESSOR 1) (MTS1). CDKX2A OR CDKX3. HOMO Saplens (Human).
CDNZ_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 36, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). FOR SAPIENS (Human).	CDN2_HDMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CMULTPLE TUMOR SUPPRESSOR 1) (MTS1). CDKNZA OR CDKNZ. HOMO SAPIENS (Human).	SULT 1 CON2_HUAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UUL-1999 (Rel. 38, Last senotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CDKN2A OR CDKN2. HOMO SAPLENS (Human).
CDM2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). HOME GRANDA (HUMAN)	CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). GORNAR OR CDKNA.	SULT 1 CDN2_HTMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1). WOME STANDARD (HUMBA)
CDN2_HUMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01.NOV-1995 (Rel. 32, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 15-UL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CDKN2A OR CDKN2.	CDN2_HDMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (MULTIPLE TUNGK SUPPRESSOR 1) (MTS1).	SULT 1 CDN2_HUAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOY-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CDKN2A OR CDKN2.
CDNZ_HUMAN STANDARD; PRT; 156 AA. P42771; 015191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 36, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CMULTIEE TUMOR SUPPRESSOR 1) (MTS1).	CDN2_HDMAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CMULTIPLE TUMOR SUPPRESSOR 1) (MTS1).	CDN2_HDAN STANDARD; PRT; 156 AA. CDN2_HDAN STANDARD; PRT; 156 AA. P42771; Q15191; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) CDKX2A OR CDKX2.
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CDN2_HUMAN ST/ P42771; Q15191;	CDN2_HUMAN STA P42771; Q15191;	SULT 1 CDN2_HUMAN ST; P42771; Q15191;
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CDN2_HUMAN STANDARD; PRT; 156 P42771: 015191:	CDN2_HUMAN STANDARD; PRT; 156 P42771: 015191:	SULT 1 CDN2_HDMAN STANDARD; PRT; 156 P4.2771: 015191:
CDN2_HUMAN STANDARD; PRT; 156	CDN2_HUMAN STANDARD; PRT; 156	SULT 1 CDN2_HUMAN STANDARD; PRT; 156
TANDARD; PRT; 156	DN2_HUMAN STANDARD; PRT; 156	1 DN2_HUMAN STANDARD; PRT; 156
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VARIANT
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  CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
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                                        MEDLINE; 96303699
                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
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/FITG-VAR 001408.

FITG-VAR 01408.

/FITG-VAR 01409.

/FITG-VAR 01410.

/FITG-VAR 01411.

/FITG-VAR 01411.

/FITG-VAR 01412.

/FITG-VAR 01412.
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"Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone families in France.";
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Five novel somatic CDNIZ/PIG mutations identified in melanoma,
Five novel somatic CDNIZ/PIG mutations identified in melanoma,
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FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS
ABILITY TO INTERACTS STRONGLY WITH CDK4 AND COULD ACT AS A NEGATIVE
REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.
SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
FUNDERASE: CDKRIAM MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A
WIDE RANGE OF TISSUES.
                                                                                                                                                                                                                                  Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
Spatz. A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
Hum. Mol. Genet. 7:941-941(1998).
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Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;
Polymorphism; 3D-structure.
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ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
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                                                                                                                                                                                                                                                                                                                                                      VARIANT PANCREATIC CARCINOMA CYS-146
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Hum. Mutat. 12:70-70(1998).
FAMILIAL MELANOMA. 98087572.
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DOMAIN 12
REPEAT 12
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Soufir N.,
VARIANTS
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Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
Richter K.H., Walker C., Baach D., Sherr C.J., Serrano M.;
"Cloning and characterization of murine plcink4a and pl5INK4b genes.";
Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
-! SUBDINT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
-! TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
-!- INDUCTION: BY TGF-BETA.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malumbres M., de Castro I., Santos J., Melendez B., Mangues R., Serrano M., Pellicer A., Fernandez-Piqueras J.; "Inactivation of the cyclin-dependent kinase inhibitor pl5INK4b by deletion and de novo methylation with independence of pl6INK4a
             WELANOMÀ).

/FITG-VAR_001414.
E -> D (IN A BILIARY TRACT TUMOR).
/FITG-VAR_001415.
L -> P (IN FAMILIAL MELANOMA).
FITG-MAR_001416.
E -> D (IN A BILIARY TRACT TUMOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B).
                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 -> P (IN FAMILIAL MELANOMA AND
                                                                                                                                                                                  Length 156;
                                                                                                                                                                                                               Indels
                                                                                                                                                                             Score 1067; DB 1; I
Pred. No. 1.98e-199;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                               121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                 121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                     ....
Note: remainder of annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                              Match 199.0%;
Local Similarity 98.7%;
les 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J X DBA;
MEDLINE; 97322242.
24
                                                                                32
                                                                                                               33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 95380169.
                                                56
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24
                                                                              32
                                                                                                             33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDN5_MOUSE
P55271;
                                                                                                                                                                              Query Match
VARIANT
                                                 VARIANT
                                                                                VARIANT
                                                                                                               VARIANT
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Matera G.A., Xiong Y.;
"Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related
CDK6 Inhibitor, correlates with wild-type pRb function.";
Genes Dev. 8:2939-2952(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAWGRLPVDLAEEQGHRDIARYLHAATG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'A cell cycle regulator potentially involved in genesis of many tumor
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE, 94359613.

Hannon G.J., Beach D.;

"PISINK4B is a potential effector of TGF-beta-induced cell cycle
                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CYCLIN-DEPENDENT KIRASE 4 INHIBITOR B (P14-INK4B)
(MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harshman K.,
                                                                                                                                Length 130;
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94204645.
Kamb A., Gruls N.A., Weaver-Feldhaus J., Liu Q., Harshmai
Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
Skolnick M.H.;
                                                       Repeat: ANK repeat.
2 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
WY, 7AADGOFF552BCFF9 CRC64;
                                                                                                                              Score 729; DB 1; L. Pred. No. 6.89e-126; 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50. MEDLINE; 95188190.
                                                                                                                                                                                                                                                                                                   138 AA
                                                                                                                                                                                                                                                                                                   PRT;
        EMBL, U66085; AAB39833.1; --
EMBL, U66084; AAB39833.1; JOINED.
MGD; MGI:1104737; CDKN2B.
PFAM; PF00023; ank; ank;
                                                                                           65 95 A
130 AA; 13788 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 53-138 FROM N.A.
                                                                                                                              Match 67.6%;
Local Similarity 88.3%;
les 106; Conservative
                                                          Cell cycle; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 264:436-440(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 371:257-261(1994).
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 95095079.
                                                                                                                                                                                                                                                                                                                                                                                    CDKN2B OR MTS2
                                                                                                                                                                                                                                                                                       CDN5_HUMAN
P42772;
                                                                                           REPEAT
SEQUENCE
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arrest.
                                                                                 REPEAT
                                                                    DOMAIN
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                                                                                                                                                      Matches
SARARATTES
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US-09-016-869A-2.rsp

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                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR. POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                  18 LASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSARVAELLLLHGAEPNCADP 77
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knapek D.F., Serrano M., Beach D., Trono D., Walker C.L.;
"Association of rat pi5inK48/pi6inK4 deletions with monosomy 5 in
kidney epithelial cell lines but not primary renal tumors.";
Cancer Res. 55:1607-1612(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE; 96001392.
Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,
Tsuchiya H., Kikuchi Y., Mitani H.;
"Molecular genetic basis of renal carcinogenesis in the Eker rat
model of tuberous solerosis (Tsc2).";
Mol. Carcinog. 14:23-27(1995).
                                                                                                                                                                                                  Repeat; ANK repeat; Disease mutation.
2 X ANK WOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
                                                                                                                                                                                                                                                 G->E (IN LONG ADENOCARCINOMA).
/FIId=VAR_001488.
/FIId=VAR_00489.
SA -> TP (IN REF. 2).
MISSING (IN REF. 2).
OLL -> HSW (IN REF. 2).
WHY (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                   Score 725; DB 1; Length 138;
Pred. No. 5.00e-125;
6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AA.
                        - I - SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                            M.
                                                                                                                                                   EMBL; U17075; AAC50075.1; -.
EMBL; L36844; AAA50282.1; -.
EMBL; S69805; AAD14049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 46-86 FROM N.A. MEDLINE; 95228036.
                                                                                                                                                                                                                                                                                                                                                                   Match 67.3%;
Local Similarity 87.5%;
les 105; Conservative
                                                                                                                                                                                                     Cell cycle; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                           14722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                              39
103
47
                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                     20
23
32
138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 96001392.
                                                                                                                                                                                                                                                                             20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDKN2B OR INK4.
                                                                                                                                                                                         MIM; 600431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 4
CDN5_RAT
P55272;
                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                              VARIANT
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                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                    -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN TESTIE, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL. KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
-1- SIMILARITY: BELONGS TO THE CDRNZ FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.; Cloning and characterization of murine pigiNK4a and pi5INK4b genes."; Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                           cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
N CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1 - SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATLITRPVHDAAREGFLDTLMVLHKAGARLDVCDAWGRLPVDLAEEGGHRDIARYLHAAIG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-CCT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4).
CDKN2A OR P16INK4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIEFRATION OF NORMAL CELLS. INHIBITS THE PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LATAAARGOVETVROLLEAGADPNAVNRFGRRPIOVMMGSAQVAELLLLHGAEPNCADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHORT FORM.
FOR THE SHORT FORM.
2 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 720; DB 1; L
Pred. No. 5.94e-124;
8; Mismatches 8;
INITIATION CODONS IN THE SAME READING FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 AA.
                                                                                                                                   -! - SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LONG FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
95
31
85
AN
13748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                      EMBL; S77734; CAB35360.1; -. EMBL; S77734; CAB33639.1; -. PFAM; PF00023; ank; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 66.8%;
Local Similarity 86.7%;
Nes 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
5
5
65
130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDITINE; 95380169.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
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P51480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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PFAM; PF00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishop D.T.;
                                                                                              VARSPLIC
                                                                                                          SEQUENCE
                                                                                                                                    Query Match
                                         REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                   CDKN2D.
                                                                                REPEAT
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Matches
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                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Sherburn T.E., Gale J.M., Ley R.D.;
Sherburn T.E., Gale J.M., Ley R.D.;
Submitted (WAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
REGIATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
-!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
INTITATION CODONS IN THE SAME READING FRAME.
-!- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
-!- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                       Repeat: ANK repeat; Alternative initiation.
4 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 3.
                                                                                                                                                                                                                                                                                                                                                                         DSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWGRLPLDLAQERGHQDIVR 119
                                                                                                                                                                                                                                                                                                                                                                                      1 MESAADRLARAA-QGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHVAALLLNYGA 59
                                                                                                                                                                                                                                                                                                                                    9 MEDSADWILATAAARGRVEEVRALILEAVALPNAPNSYGRRPIQVWMGSARVAELLLIHGA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4)
(TUMOR SUPPRESSOR CDRN2A).
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                           Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monodelphis domestica (Short-tailed grey opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
                                                                                                                                                                                                                                                                 Score 663; DB 1; Length 167;
Pred. No. 9.94e-112;
20; Mismatches 14; Indels
                                                                                                                                                                                                                            MISSING (IN SHORT ISOFORM).
88C4588A105ECB8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF064808; AAC23669.1; -. EMBL; AF064808; AAC23670.1; -.
                                                                                                                                                                                                                                      167 AA; 17870 MW;
                                                                                                      EMBL; L76150; AAA85453.1; -.
MGD; MGI:104738; CDKN2A.
PFAM; PF00023; ank; 2.
                                                                                                                                                                                                                                                                    61.5%;
                                                                                                                                               Cell cycle; Anti-oncogene;
DOMAIN 4 152
                                                                                                                                                                                                                                                                              Best Local Similarity 72.2%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                         34
66
100
152
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68
101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 YLRAAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDN2_MONDO
077617;
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REPEAT
REPEAT
REPEAT
VARSPLIC
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  69
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epeat; ANK repeat; Alternative initiation. 4 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J., Lahkin J.M., Sherr C.J., Downing J.R., "Molecular cloning, expression pattern, and chromosomal localization of human CDKNZD/INK4d, an inhibitor of cyclin D-dependent kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guan K.L., Jenkins C.W., Li Y., O'Reefe C.L., Noh S., Wu X.,
Zariwala M., Matera A.G., Xiong Y.;
"Isolation and characterization of p19INK4d, a p16-related inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                  12 SADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMMGSARVAELLLLHGAEPN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 98421670.
Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Payletich N.P.;
"Structural basis for inhibition of the cyclin-dependent kinase Cdk6
by the tumour suppressor pi6INK4a.";
Nature 395:237-243(1998).
                                                                                                                                                                                                                                                                                                                     Gaps
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Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mutation testing in melanoma families: INK4A, CDK4 and INK4D."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.
                                                                                                                                                                                                                                                                 Length 171;
                                                                                                                                                                                                                                                              Score 575; DB 1; Length 171
Pred. No. 5.27e-93;
15; Mismatches 22; Indels
                                                                                                                                                                                  MISSING (IN SHORT ISOFORM).
MW; 694264F5D0F4F6CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDN7_HUMAN STANDARD; PRT; 166 AA. P55273; Q13102; Q10-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. Cell 7:57-70(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specific to CDK6 and CDK4.";
                                                                                                                                                                                                                                                                 53.3%;
                           Cell cycle; Anti-oncogene;
DOMAIN 46 169
                                                                                                                                                                                                                                                                                       larity 69.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 29:623-630(1995).
                                                                                                                                                                                                             18707
                                                                                                     109
143
169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE; 96121373.
                                                                                                                                                                                                             171 AA;
                                                                                                                                                                                                                                                                                          Local Similarity
hes 83; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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46
111
144
144
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                                                                                                                                                                                                                                                                       Laue E.D.;
"Structure of the cyclin-dependent kinase inhibitor p19Ink4d.";
"Ature 189:999-1003(1997).
"Ature 389:999-1003(1997).
-I- FUNCIION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
-I- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 GDRLSGARARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 VQDASG-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
KINASE 4 INHIBITOR C) (P18-INK4C).
CDKN2C OR CDKN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 95095079.
Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
                                                                                                                                                                                                                                    Luh F.Y., Archer S.J., Domaille P.J., Smith B.O., Owen D.,
Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
                                                                       MEDLINE; 95257949.
Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.;
"Identification of human and mouse pl9, a novel CDK4 and CDK6
Inhibitor with homology to pi6ink4 ";
Mol. Cell. Biol. 15:2682-2688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell cycle; Anti-oncogene; Repeat; ANK repeat; 3D-structure. DOMAIN 7 137 4 X ANK MOTIF REPEATS. REPEAT 7 41 ANK MOTIF 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 341; DB 1; Length 166
Pred. No. 1.29e-44;
19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A -> P (IN REF. 2).
9E74F5C23B7EBCB2 CRC64;
cyclin D-dependent kinases CDK4 and CDK6.";
Mol. Cell. Biol. 15:2672-2681(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
                                                                                                                                                                                                                                                                                                                                                                         INHIBITORS.
-1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 41 A1
42 72 Ab
73 104 Ab
105 137 Ab
17 17 Ab
166 Aa; 17894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U19597; AAC52194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1AP7; 16-SEP-98.
MGD; MGI:105387; CDKNZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00023; ank; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 59; Conserv
                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                    MEDLINE; 98013176
                                                                                                                                                                           [3]
STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDN6_HUMAN P42773;
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                                                                         Holak T.A.;
"Structure of human cyclin-dependent kinase inhibitor pi9(INK4d):
"Structure of human ankyrin-repeat-containing structures and
implications for the dysfunction of tumor suppressor pi6(INK4a).";
Structure 6:1279-1290(1998).
-i- FUNCTION: INPERACTS STRONGLY WITH CDK4 AND CDK6.
-i- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVQDTSG-TSPVHDAARTGFLDTLKVLVEHGADVNVPDGTGALPIHLAVQEGHTAVVSFL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engh R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A X ANK MOTIF REPEATS.

ANK MOTIF 1.

ANK MOTIF 2.

ANK MOTIF 3.

ANK MOTIF 3.
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Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.8%; Score 364; DB 1; Length 166; larity 49.2%; Pred. No. 3.10e-49; Conservative 22; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> P (IN REF. 3).
2FACD11CF56340DC CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDN7_MOUSE STANDARD; PRT; 166 AA. 060773; Q60794; O1-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                                                                                                                                    -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                  X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE; 98455510.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U49399; AAB03772.1; -.
EMBL; U40343; AAB18139.1; -.
EMBL; U20498; AAA85436.1; -.
EMBL; AF061327; AAC27450.1; -.
PDB; IBI8; 16-FEB-99.
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137 AN
159 Q
1700 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00023; ank; 3.
Cell cycle; Anti-oncogene;
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STRAIN-C57BL KAPLAN;
MEDLINE; 95257948.
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105 1
159 1
166 AA;
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nes 61; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AAES 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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Matches

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2; Gaps

Length 166;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOUND IN PANCREAS AND HEART.
--- DISEASE: CDKN2C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
--- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venkataramani R., Swaminathan K., Marmorstein R.; "Crystal structure of the CDK4/6 inhibitory protein pl8INK4c provides insiphts into ankyrin-like repeat structure/function and tumor-derived pl6INK4 mutations."; Nat. Struct. Biol. 5:74-81(1998).
                 "Growth suppression by pl8, a pl6INK4/MTS1- and pl4INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb function."; Genes Dev. 8:2939-2952(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A -> P (IN BREAST CANCER; LOSS OF CDK6 INTERACTION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 99175088.
Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Maille P., Selby T.,
Tsai M.-D.;
                                                                                                                                                                  Blais A., Labrie Y., Poullot F., Lachance Y., Labrie C.;
Structure of the gene encoding the human cyclin-dependent kinase
inhibitor p18 and mutational analysis in breast cancer.";
Biochem. Biophys. Res. Commun. 247:146-153(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disease mutation; 3D-structure
                                                                                                                                                                                                                                                                                                MEDLINE; 96438606.
Lapolite J., Lachance Y., Labrie Y., Labrie C.;
"A p18 mutant defective in CDK6 binding in human breast cancer
cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR_001490.
5D66AFA715186E9A CRC64;
                                                                                                     SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 3.
ANK MOTIF 4.
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EMBL; AF041250; AAC39783.1; -.
EMBL; AF041249; AAC39783.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat;
                                                                                                                                                                                                                                                                                                                                                                                 Cancer Res. 56:4586-4589(1996).
                                                                                                                                                                                                                                                                            VARIANT BREAST CANCER PRO-72.
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PDB; 1BU9; PRELIMINARY.
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Matera G.A., Xiong Y.;
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PFAM; PF00023; ank; 3
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                                                                                                                                            MEDLINE; 98300299.
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SOLL TILITITE BRANK BRAN
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18127 MW;

168 AA;

SEQUENCE

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"Novel INK4 proteins, p19 and p18, are specific inhibitors of the
cyclin D-dependent kinases CDK4 and CDK6.";
MOI. Cell. B101. 15:2672-2681(1995).
-I- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
-I- SUBUNIT: HETERRODIMER OF P18 WITH CDK6 (BX SIMILARITY).
-I- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                   63 PDLKDRTGFA-VIHDAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEF 121
                                                                                                                          62
                                                                                                                                                       10 EPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGAE 69
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                                                                            Gaps
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                                                                                                                          3 EPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLOYA'1997 (Rel. 35, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
11-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 168;
                         Length 168;
                                                                       35; Mismatches 48; Indels
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Pred. No. 6.33e-35;
29; Mismatches 39; Indels
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ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
W; BC88D5489307E128 CRC64;
                         Score 300; DB 1;
Pred. No. 1.72e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 AA.
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MGD; MGI:105388; CDKN2C.
PFAM; PF00023; ank; 3.
                                                                                                                                                                                                                                                                                                                        122 LVKHTASNVGHRNHKGDTA 140
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                         27.8%;
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Query Match
Best Local Similarity 39.6%;
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Best Local Similarity 43.0%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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MEDLINE; 95257948.
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CDN6_MOUSE
Q60772:
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Genomics 10:858-866(1991).

Genomics 10:858-866(1991).

GENOMICS 10:858-866(1991).

GENOMICS 10:858-866(1991).

SKELETAL ELEMENTS; THEY BIND TO THE ERTHROCYTE MEMBRANE PROTEIN GP85, SMD TO THE CYTOSKELETAL PROPEINS TO CONEIN, TUBULIN, VIMENTIN AND DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES AND EXCHANGE PROTEIN;

THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES AND ACTENNIN TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES AND ACTIONS.

THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES AND EXCHANGE PROTEIN;

THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES AND ACTIONS.

THE CYTOPLASMIC DOMAIN OF THE ENTRY VARIANTS ARE PRODUCED BY ACTENDATIVE PRODUCTS: THE TWO BRAIN VARIANTS ARE PRODUCED BY ACTENDATIVE PRODUCTS: THE TWO BRAIN VARIANTS ARE PRODUCED BY ACTENDATIVE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL CELLS THROGHOUT THE BRAIN.
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                     PNLKDGTGFA-VIHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKEGHLPVVEF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92009921.
Tise W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Otto E., Kunimoto M., McLaughlin T., Bennett V.;
"Isolation and characterization of cDNAs encoding human brain ankyrins reveal a family of alternatively spliced genes.";
J. Cell Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                   ANK_BUMAN STANDARD; PRT; 1839 AA.
ANK_BUMAN STANDARD; PRT; 1839 AA.
001.405;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 32, Last annotation update)
ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing; Repeat; ANK repeat;
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ANK MOTIF 2.
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PFAM; PF00023; ank; 22.
PFAM; PF00531; death; 1.
PFAM; PF00791; 2US; 1.
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95
128
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MEDLINE; 91302466.
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TISSUE-BRAIN STEM:
MEDLINE; 91302466.
Otto E., Kunimoto M., McLaughlin T., Bennett V.;
Otto E., Kunimoto M., McLaughlin T., Bennett V.;
Isolation and characterization of cDNAs encoding human brain ankytins reveal a family of alternatively spliced genes.";
J. Cell Biol. 114:241-253(1991).
-: FONCTION: ANTYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-SKELETAL ELEMENTS; THEY BIND TO THE EXPTHROCYTE MEMBRANE PROTEIN SALETAL 2. TO NAR ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471 AARAGOVEVVRCLLRNGALVDARAREEQTPLHIASRLGKTEIVQLLLQHMAHPDAATTNG 530
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MEDLINE; 94075409.
Chan W., Kordell E., Bennett V.;
"440-kD ankyrinB: structure of the major developmentally regulated domain and selective localization in unmyellnated axons.";
J. Cell Biol. 123:1463-1473(1993).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
AUCT-1996 (Rel. 34, Last annotation update)
ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 181; DB 1; Length 183
Pred. No. 3.37e-14;
20; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5C1C1FD3D795A280 CRC64;
ANK MOTIF 3.

ANK MOTIF 4.

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nes 48; Conservative
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  Homo sapiens (Human)
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Q01484;
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                                                                                                               CELLS THROUGHOUT THE BRAIN.
PTM: PHOSPHORYLATED AT WILTIPLE SITES BY DIFFERENT PROTEIN KINASES
AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
AND FUNCTION (POTENTIAL).
SIMILARITY: CONTAINS 24 ANK REPEATS.
DESMIN. ERTTHROCTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

ALTERNATIVE PRODUCTS: THE TWO BRAIN VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING OF GENE ANK2.

TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
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ANK MOTIF 4.

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ANK MOTIF 2
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MIM; 106410; -.

MIM; 106410; -.

PROSITE; PSS0017; DEATH DOMAIN; 1.

PFAM; PF00023; ank; 2.

PFAM; PF000791; 205; 1.

Cytoskeleton; Alternative splicing; Repeat; ANK repeat;

Phosphorylation; Multigene family.

Phosphorylation; Multigene family.

REPEAT 63 95 ANK MOTIF REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 226634; CAA81387.1; -. EMBL; X56957; CAA40278.1; -. PIR; S14533; S14533. PIR; A39643.
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A BEDET S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,

Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,

Bornwell M., Herbers J.M., Kugler W., Oezcan R., Pekrun A.,

Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;

"Ankyrin-1 mutations are a major cause of dominant and recessive
Thereditary spherocytcois.";

"Ankyrin-1 mutations are a major cause of dominant and recessive
Thereditary spherocytcois.";

"Nat. Genet. 13:214-218(1996).

"In Particolous and Trach INTEGRAL MEMBRANE PROTEIN BAND 4.2, TO
ELEMENTS; BIND TO THE EXPTHROCYTE MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FOORIN, TUBULIN, VIENTIN AND DESMIN.

CRYOSKELETAL PROTEINS FOORIN, TUBULIN, VIENTIN TO THE
CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;

THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

"THEY RELIGIAN AND TOR ALL OF THESE BINDING FUNCTIONS.
                                                                                                                                                                                            AARAGQVEVVRCLLRNGALVDARAREEQTPLHIASRLGKTEIVQLLLQHMAHPDAATING 530
                                                                                                                                                                      531 YT-PLHISAREGQVDVASVLLEAGAAHSLATKKGFTPLHVAAKYGSLDVAKLLLQRRAAA 589
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                                                                                                           SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
TISSUE-HEMATOPOIETIC;
MEDINE; 90158830.
Lux S.E., John K.M., Bennett V,;
"Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle
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-1- DISEASE: DEFECTS IN ANKI ARE THE CAUSE OF DOMINANT AND RECESSIVE HERDITARY SPHEROCYTOSIS (HS).
-1- SIMILARITY: CONTAINS 24 ANK REPEATS.
                                             Gaps
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ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED
ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D., Cheung M.C., Kan Y.W., Palek J.; "cDNA sequence for human erythrocyte ankyrin."; Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Length 3924;
  Score 181; DB 1; Length 392,
Pred. No. 3.37e-14;
20; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)
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Query Match
Best Local Similarity 38.1%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             control proteins.";
Nature 344:36-42(1990).
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TVEGPLEDPSELEVDIDYFWKHSKDHTSTPNP -> ELRGS
GLQPDLIEGRKGAQIVKRASLKRGKQ (IN A THIRD
                                                                                                                                                                                                                                                              PFAM; PF00023; ank; 22.
PFAM; PF00053; deach; 1.
PFAM; PF00791; 205: 1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
Phosphorylation; Lipoprotein; Multigene family; Disease mutation;
Plosphorylation; Lapoprotein; Multigene family; Disease mutation;
Plusper Service Se
                                                                                                                                                                                                                                                                                                                                                                                                                                  89 KD DOMAIN (ANION EXCHANGE PROTEIN BINDING DOMAIN).
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24 X ANK MOTIF REPEATS.
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V -> I (IN HS).

/FTId-VAR_000596.

R -> H (IN BRUEGEN).

/FTId-VAR_000597.
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PIR; A35049; A35049.
RSSP; Q00420; IAWC.
MIM; 182900; PROSITE; PS50017; DEATH_DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                                      Gaps
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1 827 89 KD DOMAIN (ANION EXCHANGE PROTEIN
28 1386 62 KD DOMAIN (SPECTRIN BINDING
DOMAIN).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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--- PTH: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
--- PTH: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
--- SIMILARITY: CONTAINS 22 ANK REPEATS.
                                                                                                                                                                                                                 Length 1880;
                                                                                                                                                                                                            Score 174; DB 1; Length 188
Pred. No. 5.58e-13;
16; Mismatches 50; Indels
                                                                                                      A -> S (IN REF. 2).
V -> I (IN REF. 2).
W; 1C5F5E7EFDICD428 CRC64;
D -> N (IN DUESSELDORF).
/FTId=VAR_000602.
R -> D.
/FTId=VAR_000603.
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01-NOV-1995 (Rel. 32, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
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HSSP; Q00420; 1AWC.
MGJ: 88024; ANK.
PROSITE; PSS0017; DEATH_DOMAIN; 1.
PFAM; PF00023; ank; 23.
PFAM; PF00791; G15; 1.
PFAM; PR00791; Z15; 1.
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Best Local Similarity 39.0%;
Matches 46; Conservative
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TISSODE-LOWG, AND TESTIS;
MEDLINE; 9628162 H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
Uyttendaele H., Marazzi G., Wu G., Yan Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMM-GSARVAELLLLHGAEPNCAD 74
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MEDLINE; 97294599.
Gallahan D., Callahan R.;
the mouse mammary tumor associated gene INT3 is a unique member of
the NOTCH gene family (NOTCH4).";
Oncogene 14:1883-1890(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563 KNGLT-PLHVAVHHNNLDIVKLLLPRGGSP-HSP-AWNGYTPLHIAAKQNQIEVARSL 617
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SEQUENCE FROM N.A.
MEDLINE; 92194507.
Robbins J., Blondel B.J., Gallahan D., Callahan R.;
Robbins J., Blondel B.J., Gallahan D., Callahan R.;
"Mouse mammary tumor gene int-3: a member of the notch gene family transforms mammary epithelial cells.";
J. Virol. 66:2594-2599(1992).
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9131695; Q62389;
01-JUL-1993 (Rel. 26, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING
55 KD REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN O'S PECTRIN AND THE BAND 3 PROTEIN).
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Mus musculus (Mouse).
Eukaryote, Metazoa, Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 8.30e-13;
17; Mismatches 50; Indels
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:36:11 2000; MasPar time 18.43 Seconds 586.937 Million cell updates/sec Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-09-016-869A-2 (1-156) from US09016869A.pep 1078 1 MDPAAGSSWEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156

PAM 150 Gap 11 Scoring table:

225878 seqs, 69334122 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

sptrembil2
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 43.910; Variance 82.660; scale 0.531 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB ID Description Pred. No. (1) 1975.10 CELL CYCLEN BEGATIVE RE 1.35e-131 (2) 089088 CYCLIN DEPENDENT KINAS 3.53e-115 (3) 085251 P15/PGENZA/MYS1 (FRAGM 7.07e-104 (3) 0921C1 CYCLIN DEPENDENT KINAS 4.38e-95 (3) 0921C1 CYCLIN DEPENDENT KINAS 4.38e-95 (3) 0921C2 CYCLIN DEPENDENT KINAS 3.66e-90 (4) 0921C2 CYCLIN DEPENDENT KINAS 3.66e-90 (5) 097616 CYCLIN DEPENDENT KINAS 1.89e-43 (6) 097618 P13CDKNZX PROTEIN KINAS 1.89e-43 (6) 097618 CYCLIN-DEPENDENT KINAS 1.89e-43 (6) 097189 P16INK4A TUMOR SUPPRES 2.67e-17 (1) 0921C3 ALT. ANKYRIN (FRAGMENT). 1.57e-13 (1) 09107 ANKYRIN (FRAGMENT) 5.32e-13 (1) 061304 ANKYRIN 1, ERYTHROLD (7.97e-13)	æ (į					
CELL CYCLE NEGATIVE RE	Query Score Match Length DB	Lengt	:	8	ជ	Description	Pred. No.
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O921C1	596 55.3 86	86		ø	Q9XS52	_	1.66e-98
054846 CYCLIN-DEPENDENT KINAS 3. 0921C2 CYCLIN-DEPENDENT KINAS 7. 094618 P13CDKN2X. PCDEIN. 2. 095840 CYCLIN-DEPENDENT KINAS 1. 097846 CYCLIN-DEPENDENT KINAS 1. 0921E8 P16INK4A TUMOR SUPPRES 2. 0921C3 CYCLIN-DEPENDENT KINAS 1. P97582 ANKYRIN (FRAGMENT). 1. 013768 ALT. ANKYRIN (VARIANT 5. 061304 ANKYRIN I, ERYTHROID (7. 061304 ANKYRIN I, ERYTHROID (7. 088521 190 KDA ANKYRIN ISOFOR 2.	566 52.5 86	98		디	09Z1C1		4.38e-92
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P70067 CDNK2X PROTEIN. B	480 44.5 113	113	٠.	Ξ	Q921C2	×	7.77e-74
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2 CYCLIN-DPENDENT KINAS 1. 2 ANKYRIN (FRAGMENT). 1. 3 ALT. ANKYRIN (VARIANT 5. 4 ANKYRIN 1. ERYTHROID (7. 5 ANKYRIN 1. ERYTHROID (7. 6 ANKYR	198 18.4 42 1	42]	_	ᆵ	0921E8	PI6INK4A TUMOR SUPPRES	2.67e-17
ANKYRIN (FRAGMENT). 1. ALT. ANKYRIN (VARIANT 5. ANKYRIN 1, ERYTHROID (7. ANKYRIN 1, ERYTHROID (7. 190 KDA ANKYRIN ISOFOR 2.	194 18.0 42	42	٠.	디	092103	CYCLIN-DEPENDENT KINAS	1.42e-16
ALT. ANKYRIN (VARIANT 5. ANKYRIN. ANKYRIN , ERTHROID (7. ANKYRIN I, ERTHROID (7. 190 KDA ANKYRIN ISOFOR 2.		843]	_	Ξ	P97582	ANKYRIN (FRAGMENT).	1.57e-13
AMKYRIN. I AMKYRIN I, ERYTHROID (7. AMKYRIN I, ERYTHROID (7. 190 KDA ANKYRIN ISOFOR 2.	16.1	1719		4	013768	ALT. ANKYRIN (VARIANT	5.32e-13
ANKYRIN 1, ERYTHROID (7. ANKYRIN 1, ERYTHROID (7. 190 KDA ANKYRIN ISOFOR 2.	16.1	1856		4	099407	ANKYRIN.	5.32e-13
ANKYRIN 1, ERYTHROID (7.	16.0 1	1098		1	061304	'n	7.97e-13
190 KDA ANKYRIN ISOFOR 2.	16.0	1848		11	061302	Ĥ	7.97e-13
	15.8 1	1762		Π	088521	KDA	2.67e-12

2.67e-12	1.97e-11	4.36e-11	6.48e-11	6.48e-11	6.48e-11	1.43e-10	1.43e-10	1.43e-10	1.43e-10	1.43e - 10	1.43e-10	1.43e - 10	1.01e-09	2.20e-09	3.24e-09	1.03e-08	1.51e-08	3.24e-08	3.24e-08	1.47e-07	1.47e-07	3.13e-07	6.60e-07
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15.8	15.3	15.1	15.0	15.0	15.0	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.4	14.2	14.1	13.8	13.7	13.5	13.5	13.2	13.2	13.0	12.8
170		163	162	162	162	160	160	160	160	160	160	160	155	153	152	149	148	146	146	142	142	140	138
21	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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A SARTOS J., MELENDEZ B. PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
SARTOS J., MELENDEZ B. PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERAS J.;
T "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
I n mouse inbred strains.";
I submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
R EMBL; MG6087, AAC08963.1;
R EMBL; U66087, AAB39600.1;
R EMBL; U66087, AAB39600.1;
R EMBL; U660886, AAB39600.1;
R EMBL; U660886, AAB39600.1;
R EMBL; U670188, AAB39600.1;
R EMBL; U79628, AAB39600.1;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-42 FROM N.A.
STRAIN-BBA/Z AND C57BL/6;
MEDILINE; 95380169.
QUELLE D.E., ASHMUN R.A., HANNON G.J., REHBERGER P.A., TRONO D.,
RICHTER K.H., WALKER C., BEACH D., SHERR C.J., SERRANO M.;
"Cloning and characterization of murine pleinK4a and plsinK4b genes.";
Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                  HERZOG C.R., YOU M.; *Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
                                                                                                                ZHANG S., RAMSAY E.S., MOCK B.A.; "Cdkn2a, the cyclin-dependent kinase inhibitor encoding pl6INK4a and pl9ARF, is a candidate for the plasmacytoma susceptibility locus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOLOFF E.V., HERZOG C.R., YOU M.; The 5'-flanking region of the El alpha form of the murine pl6INK4a
                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J X DBA;
MALUMBRES M., DE CASTRO I., SANTOS J., MELENDEZ B., MANGUES R.,
SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-42 FROM N.A.
STRAIN-DBA/2 AND C57BL/6;
GRESSAIN K.M., ROLLINS L.A., MILLER M.S.;
Submitted (JMN-1997) to the EMBL/GenBank/DDBJ databases.
 (P16INK4A) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN)
                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89AD5E62 CRC32;
            CDKN2A OR EIALPHA OR PI6INK4A OR CDKN2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 AA; 17941 MW;
                                                                          SEQUENCE FROM N.A.
STRAIN-DBA/2N; TISSUE-SPLEEN;
MEDLINE; 98151529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD00223.1; -
                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-155 FROM N.A.
                                                                                                                                                                                                                                                                        Mamm. Genome 8:65-66(1997).
                                                                                                                                                                                             SEQUENCE OF 1-42 FROM N.A. STRAIN-VARIOUS STRAINS; WEDLINE; 97179476.
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P42771: 1B17.
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                         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                             suppressor gene.
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EMBL;
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Length 168;

DB 11;

62.9%; Score 678;

Query Match

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"Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
suppressor gene.";
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01-NOV-1998 (Tremblrel. 08, Last sequence update)
01-NOV-1999 (Tremblrel. 12, Last annotation update)
01-NOV-1999 (Tremblrel. 12, Last annotation update)
01-NOV-1999 (Tremblrel. 12, Last annotation update)
02-CLIN DEPENDENT KINASE INHIBITOR PROTEIN).
COCCLIN DEPENDENT KINASE INHIBITOR PROTEIN).
CDKNZA OR EIALPHA OR P16.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                    SEQUENCE OF 1-42 FROM N.A.
STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
"Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 049279; AAC00951.1;
EMBL; 079279; AAD00224.1;
"EMBL; 079228.
                                                                                                                     ZHANG S., RAMSAY E.S., MOCK B.A.; "Cdkn2a, the cyclin-dependent kinase inhibitor encoding pl6INK4a and pl9AFF, is a candidate for the plasmacytoma susceptibility locus, port."
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                                                                                          1 MESAADRLARAAAQGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMMGNVHVAALLLNYGA 60
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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     Pred. No. 3.53e-116;
20; Mismatches 14;
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STRAIN-BALB/CANPT; TISSUE-SPLEEN;
MEDLINE; 98151529.
Best Local Similarity 73.0%;
Matches 92; Conservative
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les 91; Conservative
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Kinase; Cyclin.
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Mammalla;

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STRAIN-SPRET/EI;
SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VMMMGSAQVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAW 60
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in mouse inbred strains."; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases. EMBL, U79637.1; AADO0237.1; -- HSSP; P42771; 1B17.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NUV-1998 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PISINK4B (FRAGMENT)
                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
U-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                       Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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111 GRLPVDLAEELGHRDVARYLRAAAG 135
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9269 MW;
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Submitted (JUL-1997) to the
EMBL; AF015460; AAB94534.1;
HSSP; P42771; 1B17.
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91.8%;
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92.9%;
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les 79; Conservative
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les 78; Conservative
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                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
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SEQUENCE
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                                                                                  RESULT 6
ID Q9Z1C1
AC Q9Z1C1;
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054846
054846;
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Matches
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OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
"Cloning and chromosomal mapping of the felline genes p16(MTS1/CDKNZA)
and p15(MTS2/CDKNZB).";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010807; BAA33540.1; -.
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OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
NISHIGARI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
"Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKNZA)
and p15(MTS2/CDKNZB).";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010808; BAA33541.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VMMMGSARVAELLLLHGADPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VMAMGSARVAELLLLHGADPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 60
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
p15/MTS2/CDKN2B (FRAGMENT).
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
P16/CDKN2A/MTSI (FRAGMENT).
Fells silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Carnivora; Fissipedia; Felidae; Felis.
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Pred. No. 1.66e-98;
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                                                                                                                                                                       102 AA.
                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.3%;
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Matches 86; Conservative
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Matches 83; Conservative
                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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121 YLRSAG 126
                                                   129 YLRAAA 134
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SEQUENCE
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                                                                                                                                               LT 4
Q9XS51
Q9XS51;
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09XS52;
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Gaps ö

Score 566; DB 11; Length 86; Pred. No. 4.38e-92; 4; Mismatches 2; Indels

86 AA.

PRT;

D5811BE2 CRC32;

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Gaps

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Length 86;

Score 557; DB 11; Length 86; Pred. No. 3.66e-90; 5; Mismatches 2; Indels

FEC97F63 CRC32;

EMBL/GenBank/DDBJ databases

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Gaps

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LT 8 Q9Z1C2 Q9Z1C2;

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SEQUENCE FROM N.A.

ESGLA AC 090 PD 100 PD 100

STRAIN-SPRET/EI

Kinase; Cyclin. NON_TER 113 SEQUENCE 113 A

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Xiphophorus helleri.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Buteleostei; Acanthopterygil; Atherinomorpha;
Cyprinodontiformes; Cyprinodontoidei; Poeciliidae; Xiphophorus.
                                                              LITAAAKGHTAEVEALLLQGAPVNGVNSFGRRAIQVMMMGSSEVARLLLIRGADPNVIDK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LTTAAAKGHTAEVEALLLQGAPVNGVNSFGRRAIQVMMMGSSEVARLLLTRGADPNVTDK 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROBERTSON K.D., JONES P.A.;
"Tissue-specific alternative splicing in the human INK4a/ARF cell
cycle regulatory locus.";
Oncogene 0:0-0(1998).
EMBL; AF115544; AAD11437.1; -.
HSSP; P42771; 1B17.
                                                                                                                                           67 STGATPLHDAARTGFLDTVQLLVKAGADPQARDKDNCLPIDLARQNGHTDVVAVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 STGATPLHDAARTGFLDTVQLLVEAGADPQARDKDNCLPIDLARQNGHTDVVAVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-RIO SARABIA,
RAZIANIS S., MORIZOT D.C., DELLA COLETTA L., JOHNSTON D.A.,
WOOLCOCK B., VIELKIND J.R., NAIRN R.S.;
"Comparative Structure and Characterization of a CDKN2 Gene in
XIPPhophorus FISH Melanoma Model.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF132500; AAD21313.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 124;
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Best Local Similarity 55.7%; Pred. No. 2.22e-51;
Matches 64; Conservative 18; Mismatches 33; Indels
Indels
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Last annotation update)
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Last annotation update)
19; Mismatches 32;
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Pred. No. 1.89e-43;
5; Mismatches 6;
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01-MAY-1999 (TrEMBLrel. 10, Last seque
01-NOV-1999 (TrEMBLrel. 12, Last annot
CYCLIN-DEPENDENT KINASE INHIBITOR P12.
                                                                                                                                                                                                                                                                                     Created)
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Best Local Similarity 82.0%;
Matches 50; Conservative
64; Conservative
                                                                                                                                                                                                                                                PRELIMINARY;
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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Q9W6I8
Q9W6I8;
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STRAIN-JP 163 A; TISSUE-MUSCLE;
MEDLINE; 97075115.
NAIRN R.S., KAZIANIS S., MCENTIRE B.B., DELLA COLETTA L., WALTER R.B.,
MORIZOT D.C.;
                                                                                                                                                                                                                                                                                                                                               SANTOS J., WELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M., PELALANDEZ-PROUERAS J.;
PELLALCER A., FERNANDEZ-PROUERAS J.;
"COmparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: 079634; AAD00236.1; --
EMBL: 97771; 1817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xiphophorus maculatus (Southern platyfish).
Eukaryota, Metazao; Chordata; Cranlata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Acanthopterygil; Atherinomorpha;
Cyprinodontiformes; Cyprinodontoidel; Poecillidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VMMMGNVHVAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A CDKN2-like polymorphism in Xiphophorus LG V is associated with UV-B-induced melanoma formation in platyfish-swordtail hybrids."; Proc. Natl. Acad. Sci. U.S.A. 93:13042-13047(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                      Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 480; DB 11; Length 113
Pred. No. 7.77e-74;
14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAZIANIS S., NAIRN R.S.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL: U69273; AAB09560.3; -.
HSSP: P42771; 1B17.
                                                                                                                                         01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 113 113 113 113 AW; 1D82E6DF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BFB0B9C5 CRC32;
                                                                                 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AA
                                                                                                                        Created)
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
111 GRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 GRLPVDLAEELGHRDVARYLRAAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRLPLDLAQERGHQDIVRYLRSAG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 AA; 13034 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TrEMBLrel. 02, 01-MAY-1999 (TrEMBLrel. 10, 01-NOV-1999 (TrEMBLrel. 12, CDNK2X PROTEIN.
                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
44.5%;
Best Local Similarity 73.8%;
Matches 62; Conservative
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P70067 P70067;

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Best Local Similarity

SEQUENCE Query Match

REVISIONS

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436 AARAGEVEVVRCLLRNGALVDARAREEQTPLHIASRLGKTEIVQLLLQHMAHPDAATTNG 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AAR-GRVEEVRALLEAVALDNAPNSYGRRPIQYM-MMGSARVAELLLHGAEPNCADPAT 77
                                                                                                                                                                                                                                                                                                                  Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
STRAIN-WISTAR, TISSUE-BRAIN;
COSENTINO M.T., JONES O.T.;
SUDMITTED (1904-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U65916; AAB47551.1; -.
HSSP; 000421; IANC.
PFAM; PF00023; ank; 22.
NON_TER
                                                                                                                                                                                                         01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 194; DB 11;
Pred. No. 1.42e-16;
7; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    843 AA; 89982 MW; D89BDC46 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A405580F CRC32;
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                                                                                                                                                                                      Created)
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P97582
P97582
01-MAY-1997 (TrEMBLEEL 03, C3
01-MAY-1997 (TrEMBLEEL 03, L6
01-MOV-1999 (TrEMBLEEL 03, L6
MIXTRIN (FRAGMENT).
RATTUS norvegicus (RAI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase; Cyclin.
NON_TER 42 42
SEQUENCE 42 AA; 4416 MW;
                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.0%;
Matches 29; Conservative
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           843
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-SKIN;
RIEDER S., CHECA-CORTES M.L., JOERG H., STRANZINGER G.;
An equine sequence homologous to cyclin-dependent kinase inhibitor (CDKNZA).";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, RF076782; AAC97110.1;
Kinase; Cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A/J, A/WY, AKR/J, SJL/J, SWR/J, ST/J, LP/J, LS/IBG, SM/J, HS/IBG, B10;
HERZOG C.R., YOU M.;
"Polymorphisms and chromosomal mapping of the murine pl6INK4a tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 PNGVNGFGRRPIQVMMMGSVHVAELLLLHGADPNRADPDTLTRPVHDAAREGFL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eguus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Perissodactyla; Eguidae; Eguus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 suppressor gene.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: 051567, AAD09455.1; -.
HSSP; Q60773; 1AP7.
                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE 2A INHIBITOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
P16INK4A TUMOR SUPPRESSOR PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MESAADRLARAAQGRVHDVRALLEAGVSPNAPNSFGRTPIQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 330; DB 6; 1
Pred. No. 7.63e-43;
5; Mismatches 4;
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42 AA; 4402 MW; 3CA62FIF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE8139C2 CRC32;
                                                                                                                                                                                                                                                                                         58 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 58
58 AA; 6162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.6%;
Best Local Similarity 83.3%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                            PRELIMINARY;
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SEQUENCE FROM N.A.
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Length 42; 6; Indels 4

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Query Match

Matches

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Search completed: Thu Jul 20 08:36:32 2000 Job time: 21 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:38:10 2000; MasPar time 6.72 Seconds 483.073 Million cell updates/sec Tabular output not generated. Run on:

>US-09-016-869A-4
(1-137) from USO9016869A.pep
977
1 MREBNKGMPSGGGSDEGLAT.....LAEERCHRDVAGYLRTATGD 137 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq36 1:geneseqp Database:

Mean 30.377; Variance 133.757; scale 0.227 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	No.	.75	.75	.75	.75	.75	-75	-74	-65	-59	.59	-53	.53	53	-53	-53	53	-53	-53	-53	-53	-53	.53	-53
	Pred. No	3.58e-7	3.58e-7	3.58e-7	3.58e-7	3.58e-7	3.58e-7	5.05e-7	1.33e-65	1.09e-5	6.31e-5	1.66e-5	1.66e-5	1.66e-5	1.66e-53	1.66e-5	1.66e-53	1.66e-53	1.66e-5	1.66e-5	1.66e-53	1.66e-53	1.66e-53	1.66e-5
ı.	Description	Human multiple tumour	Multiple tumour suppre	Amino acid sequence 2	A human multiple tumou	Human multiple tumour		Cell-cycle regulatory	Cell-cycle regulatory	Cell-cycle regulatory	Mouse multiple tumour	Human multiple tumour	A human multiple tumou	Tumour suppressor p16.	Amino acid sequence of	Human MTS1 protein.	Truncated p27/p16 fus1	Truncated p27/p16 fus1	Truncated p27/p16 fusi	_	7 fusion	CDK inhibitory fusion	Human p16(GS)p27 fusio	
	Ą	R80948	R81702	W74553	W80526	W19255	W40526	R85117	R85115	R85118	W70823	W19251	W80524	W10627	W74549	W40524	W95105	W95106	W95103	W95096	W95107	W23536	W95095	W23535
	DB	Н	-	ч	-	-	Н	ч	Н	Н	Н	-	Ч	-	Н	-	Н	Н	Н	-	Н	Н	Н	-
	Query Match Length DB	138	138	138	138	138	138	138	138	130	130	156	156	156	156	156	237	252	334	365	365	365	380	380
æ	Query	94.1	94.1	94.1	94.1	94.1	94.1	92.8	83.8	77.5	76.7	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8
	Score	919	919	919	919	919	919	907	819	757	749	692	692	692	692	692	692	692	692	692	692	692	692	692
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48e-	48e-5	48e-	48e-5	48e-	.48e-5	.84e-	.82e-5	.31e-5	3e-4	3e-4	3e-4	3e-4	3e-4	.73e-4	3e-4	.20e-4	1e-	.85e-3	5e-	3e-	3e-
1.4	1.4	1.4	1.4	1.4	1.4	80	9	1.3	3.7	3.7	3.7	3.7	3.7	3.7	3.7	1.2	6.7	8	8		2.3
Multiple tumour suppre	ú	Inhibitor of cyclin de	Cell-cycle requlatory	Human p27-p16 fusion p	y fusion	Human multiple tumour	Human multiple tumour	Truncated p27/p16 fusi	Amino acid sequence 1	Multiple tumour suppre	A human multiple tumou	Human MTS1E1-beta prot	Human multiple tumour	Human multiple tumour	Mouse multiple tumour	Cell-cycle regulatory	Human INK4a-p16 C-term	Murine INK4a-p16 C-ter	Cell-cycle requlatory		Cell-cycle regulatory
R81701	R80940	R53401	R85116	W95094	W23534	W19252	W19253	W95104	W74550	R81700	W80525	W40525	R80947	W19254	W80527	R85114	W16324	W16322	R85120	R85113	R85119
-	Н	-	Н	Н		Н	-	Н	Н	Н	1	 1	н	н	н	Н	н	Н	-	н	н
148	148	151	156	391	391	156	156	348	105	105	105	105	105	105	168	157	67	125	125	82	127
8.69	8.69	8.69	Ġ.	ď	8.69	σ,	6	 	58.5	ω.	58.5	ъ.	8	ω.	æ	56.9	49.5	48.3	48.3	45.6	45.6
682	682	682	682	682	682	681	675	672	572	572	572	572	572	572	572	556	484	472	472	446	446
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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07-JUN-1995; US-480810.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; WO-U03316.
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28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS
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WPI; 99-044585/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1998
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                                                                                                                                                                                                                                                                                                                       Kamb A;
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Matches
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R 18-MAR-1994; UG-214582.

R 18-MAR-1994; UG-215086.

R 14-APR-1994; UG-215086.

R 14-APR-1994; UG-215086.

R 14-APR-1994; UG-227369.

R 14-APR-1994; UG-227369.

R 14-APR-1994; UG-227369.

R 14-APR-1994; UG-227369.

R 14-APR-1994; UG-215086.

R 14-APR-1994; UG-215186.

R 14-APR-1994; UG-216186.

R 14-APR-1994; UG-216186.

R 14-APR-1994; UG-216186.
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                                                                                                                      60 VAELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 119
                                                                                  VAELLLIHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
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       1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMMGSAR 59
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04-DEC-1998 (first entry)
Amino acid sequence 2 of the multiple tumour suppressor MTSIEIS.
Amintiple tumour suppressor; MTSIEIS; human; cancer; hybridisation;
somatic mutation; gene therapy.
Homo sapiens.
USS801236-A.
01-SEP-1998.
07-JUN-1995; 480810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-1996 (first entry)
Multiple tumour suppressor 2 (MTS2) polypeptide.
Multiple tumour suppressor; MTS2; cancer; diagnosis; assay; predisposition; melanoma; leukaemia; lymphoma; prognosis; predisposition; melanoma; leukaemia; lymphoma; prognosis; Homo saplens.
W09525813-Al.
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Pred. No. 3.58e-75;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R81702 standard; Protein; 138 AA. R81702;
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W74553 standard; Protein; 138 AA
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Local Similarity 95.7%;
les 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 EERGHRDVAGYLRTATGD 138
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Matches
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ID W7
AC W7
AC W7
DD DD AM
KW MCW MCW
CW SC
OS HC
PD D1
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mutation(s)
Sizolosure; Fig 11; 73pp; English
This is the amino acid sequence of the multiple tumour suppressor
This is the amino acid sequence of the invention. The MTS gene
(MTSIELS) protein, used in the method of the invention. The MTS gene
is useful in the diagnosis and prognosis of human cancer, e.g. by
strandard nucleic hybridisation techniques, of patient samples. The
mutated sequences are those that are present in somatic mutations
of the gene in cancers. The vectors can be used for gene therapy
strategies to replace function of mutated protein in patients. These
can also be used to construct protein mimetics, also for therapeutic
strategies. In addition the expression constructs can also be used
for recombinant production of MTS. Recombinant MTS can be used to
screen for drugs to be used for cancer therapy, and the protein
itself may also be used to restore MTS function in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 VAELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAELLLIHGAEPNCADPATLITRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
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Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 94.1%; Score 919; DB 1; Length 138; Local Similarity 95.7%; Pred. No. 3.58e-75; nes 132; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-1999 (first entry)
A human multiple tumour suppressor 2 (MTS2) protein.
Human; multiple tumour suppressor 1 gene; MTS1; cancer
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W80526 standard; Protein; 138 AA.
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R85117 standard; Protein; 138 AA.
                                                                                                                    (MYRI-) MYRIAD GENETICS INC.
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01-MAR-1996 (first entry)
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WPI; 95-373798/48.
        14 - APR-1998.
07 - UNN-1995; 487033.
07 - UNN-1995; US-487033.
18 - MAR-1994; US-215086.
18 - MAR-1994; US-215086.
18 - MAR-1994; US-215087.
14 - APR-1994; US-227369.
01 - UNN-1994; US-227369.
                                                                                                                                            WPI; 98-250421/22.
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                                                                                  1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMGSAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MREENKGMPSGGGSDEGLASAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human MTS2 protein.
MTS2; multiple tumour suppressor; diagnosis; cancer;
germ-line mutation; familial melanoma locus; MLM; predisposition.
                                                                                                                                                                                                                                                                10-SEP-1997 (first entry)
Human multiple tumour suppressor 2 gene product.
Human; multiple; tumour; suppressor; MTS2; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - for
                     Score 919; DB 1; Length 138;
Pred. No. 3.58e-75;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.1%; Score 919; DB 1; Length 138; 95.7%; Pred. No. 3.58e-75; vative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mutant multiple tumour suppressor gene sequences - f
production of recombinant mutant polypeptide(s)
Disclosure; Columns 73-74; 72pp; English.
The present sequence the human multiple tumour suppressor
(MTS2) gene product, useful in cancer diagnosis.
Sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skolnick MH;
                                                                                                                                                                                                                  LT 5
W19255 standard; Protein; 138 AA.
W19255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .T 6
W40526 standard; Protein; 138 AA.
W40526;
15-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                   18-MAR-1994; 214582.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215086.
14-APR-1994; US-227369.
01-JUN 1994; US-227369.
01-JUN 1994; US-251938.
17-MAR-1995; WO-003337.
07-JUN 1995; US-251938.
07-JUN 1995; US-251938.
07-JUN 1995; US-27414177.
(MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cannon-Albright LA, Kamb A, WPI; 97-258217/23.
                      94.1%;
95.7%;
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                                 Best_Local Similarity 95.7%;
Matches 132; Conservative
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Matches 132; Conservative
138
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                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                             29-APR-1997
Sequence
                      Query Match
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DNA specific for Multiple Tumour Suppressor IE1-beta gene - are useful for the diagnosis of cancers related to MTSIE1-beta mutation(s) and their treatment mutation(s) and their treatment bisclosure; Fig il; 72pp; English.

This sequence represents a human multiple tumour suppression protein, mTS2. The MTS gene locus is also referred to as the familial melanoma (MLM) genes can be used in the diagnosime 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemla, astrocytoma, gliboblastoma, lymphoma, GLL, and cancers of the pancreas, breast, thyroid, sequence 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell-cycle regulatory protein p15.
Cell-cycle regulatory p16.
Cell-cycle reg
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NP-PSDB; 75-75-75-75.

New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.

Claim B; Page 78: 109pp; English.

The human cell-cycle regulatory (CCR) protein p15 (R85117) was obtd. by expression of a cDNA clone (T02963) isolated from transforming growth factor-stimulated HeCaT cells. CCR p15 specifically inhibits the activity of cyclin-dependent kinases during various stages of the cell cycle, and can be used in the treatment and diagnosis of proliferative disorders.
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94.1%; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels
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Sequence
                                                                             Query Match
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WPI; 95-373798/48.

New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.

Claim 16; Page 87-88; 109pp; English.

A homologue (R85115) of the human cell-cycle regulatory (CCR) protein
                                                                                                                                                                                                                           60 VAELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell-cycle regulatory protein p15 homologue.
Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
CCR; cell proliferation; agonist; antagonist.
                                                                                                                                                                                                   61 VAELLLLHGAEPNCADPATLTRPVHDAARERFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
                                                                                                                                          1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRALQVMMGSAR 59
                                                                                                                     1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60
                                                                             Gaps
                                                                             1;
                                   Score 907; DB 1; Length 138;
Pred. No. 5.05e-74;
3; Mismatches 3; Indels
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note= "unidentifled amino acids"
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57. .59
/note= "unidentified amino acids'
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note= "unidentified amino
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R85115 standard; Protein; 138 AA.
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25-MAY-1994; US-248812.
14-SEP-1994; US-306511.
29-NOV-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
                                     92.8%;
                                                                                                                                                                                                                                                                                   EERGHRDVAGYLRTATGD 138
                                                                                                                                                                                                                                                                                                           EERGHRDVAGYLRIATGD 137
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                             Query Match 92.8%;
Best Local Similarity 94.9%;
Matches 131; Conservative
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14-APR-1995; U04636.
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  138 AA;
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Sequence
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pl5, showing at least 60% homology to pl5 (R85117), functions as either an agonist or antagonist of cell cycle regulation. Sequence 138 AA;
                                                                                                                                                                                                                                                                                         63 EPNCADPATLIRPVHDAAREGFLDTLVVLHRAGARLDVCDAWGRLPVDLAEEQGHRDIAR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell-cycle regulatory protein p15.
Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
CCR; cancer; cell proliferation.
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                                                                                                                                                                                                                         1 MREENKGMPSGGGSDEGLATPARGLVEKVRHSWEAGADPNGVNRFGRRAIQVWMMGSARV 60
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Claim 9; Page 81-82; 109pp; English.
The mouse cell-cycle regulatory (CCR) protein p15 (R85118) was obtd. by expression of a CDNA clone (T02964) isolated from mouse embryonal carcinoma cells. CCR p15 specifically inhibits th activity of cyclin-dependent kinases during various stages of the cell cycle, and can be used in the treatment and diagnosis of proliferative disorders.
                                                                                                                                                                                                1 MREENKGMPSGGGSDEGLATPARGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMGXXXV
                                                                                                Length 138;
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Pred. No. 1.09e-59;
10; Mismatches 7; Indels
                                                                                             Score 819; DB 1; Length 138 Pred. No. 1.33e-65; 0; Mismatches 23; Indels
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W70823 standard; Protein; 130 AA.
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R85118 standard; Protein; 130 AA.
R85118;
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14-SEP-1994; US-306511.
29-NOV-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
                                                                                                83.8%;
larity 82.6%;
Conservative
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Best Local Similarity 85.9%;
Matches 110; Conservative
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03-FEB-1999 (first entry)
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US-248812.
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                                                                                                                         Best Local Similarity
Matches 114; Conser
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WPI; 95-373798/48.
N-PSDB; T02964.
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Expression construct contg. DNA for tumour suppressor p16 - to restore p16 activity to transformed cells, useful for treating lung or bladder cancer or melanoma Disclosure; Fig 1b; 92pp; English.

This sequence represents the tumour suppressor p16. The DNA encoding this sequence is joined to a promoter functional in eukaryotic cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour suppressor p16.

Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;

Cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
anti-anglogenic activity; hyperproliferative disorder.

Homo saplens.
                                                                                                                       135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a human multiple tumour suppressor I (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 ATLITRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                       76 AILTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG
                                                                                                                                                       18 LAIPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVWWGSARVAELLLLHGAEPNCADP
                                  LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match

70.8%; Score 692; DB 1; Length 156; Best Local Similarity 85.8%; Pred. No. 1.66e-53; Matches 103; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                             W80524;
03-FEB-1999 (first entry)
A human multiple tumour suppressor 1 (MTS1) protein.
Human; multiple tumour suppressor 1 gene; MTS1; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Columns 65-66; 80pp; English.
                                                                                                                                                                                                                                                                        T 12
W80524 standard; Protein; 156 AA.
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W10627 standard, Protein, 156 AA.
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17-JUL-1996; U11787.
17-JUL-1995; US-502881.
(TEXA) UNIV TEXAS SYSTEM.
JIN X, ROLH J;
WPI: 97-133336/12.
N-PSDB; T60951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1998.
28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS INC
JAMP, 99-044585/04.
N-PSDB; V70583.
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28-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo saptens.
US5843756-A.
      16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAWGRLPVDLAEEQGHRDIAR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 GGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQYMMGSARVAELLLLHGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GGSSDAGLATAAARGQVETVRQLLEAGADPNALNRFGRRPIQVMMGSAQVAELLLLHGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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    useful for primer

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
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Human multiple tumour suppressor 1 gene product.
Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s) Claim 1; Columns 61-64; 72pp; English.
The present sequence the human multiple tumour suppressor 1 (MTS1) gene product, useful in cancer diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 749; DB 1; Length 130;
Pred. No. 6.31e-59;
11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 156;
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Mouse multiple tumour suppressor 2 (MTS2) protein.
Murine; multiple tumour suppressor 2 gene; MTS2; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 692; DB 1; I
Pred. No. 1.66e-53;
6; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                   Mouse multiple tumour suppressor gene segment
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                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Fig 19; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W19251 standard; Protein; 156 AA.
                                                                                                                                             28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-877033.
(MYRIAD GENETICS INC.
Jiang P, Kamb A, Stone S;
WPI: 99-044585/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UTAH ) UNIV UTAH RES FOUND.
Cannon-Albright LA, Kamb A,
WPI: 97-258217/23.
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|larity 85.8%;
| Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.2%;
Matches 109; Conservative
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(UTAH ) UNIV UTAH RES FOUND
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18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

18-MAR-1994; US-227369.

14-RR-1994; US-227369.

01-UUN-1994; WO-U03537.

07-UN-1995; US-474177.
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tes 103; Conserv
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| 130 YLRTATGD 137
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                                                                                                                                                                                                                                                                                                                                N-PSDB; V7
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Best Loca Matches

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Disclosure; Column 63-64; 73pp; English.

This is the amino acid sequence of the multiple tumour suppressor 1

This is the amino acid sequence of the multiple tumour suppressor 1

(MTS-1) protein, used in the method of the invention. The MTS gene

(MTS-1) protein, used in the method of the invention. The WTS gene

(Standard nucleic hybridisation techniques, of patient samples.)

The MTS are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mineries, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein sequence 156 AA;
used in the expression construct of the invention. pl6 is an inhibitory actually, which is involved in the control of cyclin-dependent kinase 4 activity, and functions as a tumour suppressor. By detected whis sequence or the DNA encoding it, cancer cells can be detected. When the nucleic acid molecule is in the sense orientation, the expression construct can be used to restore pl6 function in a cell, particularly by reversing the transformed phenotype in tumours, especially lung or bladder cancer or melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the nucleic acid molecule is inscrted in the antisense orientation, the expression construct inhibits acid, may be diagnostic of tumours, e.g. by southern or Northern blot, antibody immunoblot, fluorescent cell sorting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 LAIPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMGSARVAELLLLHGAEPNCADP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1998 (first entry)
Amino acid sequence of multiple tumour suppressor 1.
Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation; somatic mutation; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 692; DB 1; Length 156;
Pred. No. 1.66e-53;
6; Mismatches 10; Indels
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Kamb A;
WPI; 98-494842/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.8%;
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or immunoassay
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US5801236-A.
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Human MTS1 protein.
MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
familial melanoma locus; MLM; predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA specific for Multiple Tumour Suppressor IEI-beta gene - are useful for the diagnosis of cancers related to MTSIEI-beta mutation(s) and their treatment Disclosure; Column 63-64; 72pp; English.

This sequence represents a human multiple tumour suppression protein, MTSI. The MTS gene locus is also referred to as the familial melanoma (MLM) genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukementa, astrocytoma, gliboblastoma, lymphoma, gliona, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
                                                                                                                              76 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
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                                      LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADP 75
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   LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADP
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W40524 standard; Protein; 156 AA.
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Best Local Similarity 85.8%;
Matches 103; Conservative
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15-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN 1995; US-487033.

18-MAR-1994; US-21586.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-JUN-1994; US-227369.

17-MAR-1995; WO-U03316.
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N-PSDB; V11238.
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Gaps

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Score 692; DB 1; Length 156; Pred. No. 1.66e-53; 6; Mismatches 10; Indels

Query Match 70.8%; Best Local Similarity 85.8%; Matches 103; Conservative

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:40:10 2000; MasPar time 5.21 Seconds 379.758 Million cell updates/sec Run on:

>US-09-016-869A-4 (1-137) from US09016869A.pep 977 Tabular output not generated. Title: Description: Perfect Score: Sequence:

1 MREENKGMPSGGGSDEGLAT.....LAEERGHRDVAGYLRTATGD 137

PAM 150 Gap 11 Scoring table:

145341 segs, 14437480 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1 Database:

Mean 28.536; Variance 128.899; scale 0.221 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	2.17e-79	2.17e-79	1.06e-77	5.92e-74	5.92e-74	5.92e-74	5.92e-74	5.92e-74	5.92e-74	5.92e-74	5.92e-74	5.92e-74	5.92e-74	5.92e-74	1.32e-64	7.98e-59	7.98e-59	7.98e-59	4.44e-58	8.82e-53	8.82e-53	8.82e-53	8.82e-53
		Applicatio	Applicatio	Applicatio	Applicatio	16, Applicati	Æ,	5, Applicati		16, Applicati		5, Applicati	4			3, Applicati	, Applicatio	, Applicatio	, Applicatio	7, Applicati	, Applicatio	, Applicatio	Applicatio	, Applicatio
	Description	Sequence 4,	Sequence 4'	Sequence 6,	Sequence 4,			Sequence 16	Sequence 1(Sequence 4,		Sequence 1	Sequence 1:	Sequence 8	Sequence 8	Sequence 8	4	Sequence 2	Sequence 2	Sequence 2	Sequence 2
SUMMARIES	er er	US-08-306-	US-08-893-	PCT-US96-0	PCT-US95-0	US-09-120-	US-08-581-	US-08-486-	US-08-508-	US-08-480-	US-08-384-	US-08-474-	US-08-627-	US-08-848-	US-08-487-	US-08-581-	PCT-US95-0	US-08-627-	US-08-581-	US-08-508-	US-08-480-	US-08-474-	US-08-487-	US-09-120-
	DB	7	0	4	❖	ო	m	7	~	-	m	-	~	~	н	ო	4	~	ო	~	Н	-	ч	m
	Match Length DB	137	137	136	138	138	138	138	138	138	138	138	138	138	138	138	130	130	130	130	156	156	156	156
a 0.00	Match	100.0	100.0	98.2	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	83.8	77.5	77.5	77.5	7.97	70.8	70.8	70.8	70.8
	Score	977	977	959	919	919	919	919	919	919	919	919	919	919	919	819	757	757	757	749	692	692	692	692
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692 70.8 156 2 US-08-508- Sequence 2, Applicatio 8.82e-53 70.8 156 2 US-08-686- Sequence 2, Applicatio 8.82e-53 16 2 US-08-686- Sequence 2, Applicatio 8.82e-53 18 18 4 PCT-0S93-0 Sequence 4, Applicatio 7.48e-52 18 18 3 US-08-384- Sequence 16, Applicatio 7.48e-52 18 18 1 US-08-184- Sequence 24, Applicatio 7.48e-52 18 1 US-08-184- Sequence 2, Applicatio 7.48e-52 18 18 1 US-08-18-18- Sequence 2, Applicatio 7.48e-52 18 18 18 18 18 18 18 18 18 18 18 18 18	ALIGNMENTS THE STANDARD: PRT; 137 AA. Sequence 4, Application US/08306511A Septicant: Seaton Seaton Sequence Sequence 4, Application US/08306511A SPELICANT: Beach, Manuel APPLICANT: Beach, Manuel APPLICANT: Seaton Manuel CITY: Boscon STREES: ADDRESSE: LANIVE & COCKFIELD COMPRESSE: LANIVE & COCKFIELD CITY: Boscon CONTRY: USA COMPUTER: IBM FC Competible COMPUTER: IBM FC COMPATION: MEDITY: BOSCON MANUER: SACIICANTON DATA: COMPUTER: IBM FC COMPATION: APPLICANTON NUMBER: 16,709 REGISTRATION NUMBER: 16,709 REGISTRATION NUMBER: 16,709 REGISTRATION NUMBER: 16,709 REGISTRATION FOR SEGID NO: 4: SEQUENCE CHARACTERISTICS: LEBSCTH: 137 anno acids TYPELCONGUL TYPE: protein
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US-09-016-869A-4.rai

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NAME: Vincent, Matthew P
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                                                                                                                                                                61 AELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAE 120
                                                                                                              1 MREENKGMPSGGGSDEGLATPARGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMMGSARV 60
                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08893274
Patent No. 596881.
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, TITLE OF INVENTION: and Uses Related Thereto NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                             Score 977; DB 2; Length 137;
Pred. No. 2.17e-79;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCIILER; C. DOJAS DOS SOFTWARE: ASCIILERX1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-UULY-1997
CLASSIFICATION DATA:
APPLICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: FOLEY, HOAG & BLIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                  PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
137 AA; 14746 MW; 80670 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08893274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                             Query Match
Best Local Similarity 100.0%;
Matches 137; Conservative
                                                                                                                                                                                                                               121 ERGHRDVAGYLRTATGD 137
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US-08-893-274-4
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SEQUENCE
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                                                                                                                                                                                                                                                                     Length 137;
                                                                                                                                                                                                                                                                     Score 977; DB 2; Length 137 Pred. No. 2.17e-79; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05252
FILING DATE: NOT yet assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application PC/TUS9605252
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: p19: A Cell Cycle Inhibitor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICEATION DATA:
APPLICATION NUMBER: US 08/425,093
FILING DATE: 17-APR-1995
ATTOKNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 02307B-059910PC
REFERENCE/DOCKET NUMBER: 02307B-059910PC
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 AA
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMUNICATION INFORMATION:
TELEPRONE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 137 AA; 14746 MW; 80670 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application PC/TUS9605252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: One Market F
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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SECUENCE

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1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVWMMGSAR 60
                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,130
                                                                                                                                                                                                                                                                           138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/217,562
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09120130
Patent No. 6037462
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09120130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 118-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                               121 EERGHRDVAGYLRTATGD 138
                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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US-09-120-130-16
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                                                                                                                                                                                                                                                                                                           60 AELLLIHGAEPNCADPATLIRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAE 119
                                                                                                                                                                                                                                           TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04636
                                                                                                                                                                           Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 138;
                                                                                                                                                                           Query Match 98.2%; Score 959; DB 4; Length 136
Best Local Similarity 99.3%; Pred. No. 1.06e-77;
Matches 136; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                            NAME/KEY: Protein
LOCATION: 1.136
OTHER INFORMATION: /note= "human pl5"
KCE 136 AA: 14689 MW; 79498 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/306,511
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-NAY-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: APPLICATION ACIDS
TYPE: APPLICATION ACIDS
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.1%; Score 919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application PC/TUS9504636
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
ENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application PC/TUS9504636
LENGTH: 136 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                             TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                        120 ERGHRDVAGYLRTATGD 136
                                                                                                                                                                                                                                                                                                                                                                                          121 ERGHRDVAGYLRTATGD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
               TYPE: amino
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 4
PCT-US95-04636-4
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RESULT

SEQUENCE Query Match

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SEQUENCE
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Patent No. 6043030
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Servano, Manuel J.
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
                                                                                                                                      61 VAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
                                                                                                       1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60
                                                                             1; Gaps
                                                          Score 919; DB 3; Length 138; Pred. No. 5.92e-74; 3; Mismatches 2; Indels
                                                                                                                                                                                                                  138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Worded
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION NUMBER: US 08/36,147
FILING DATE: 23-NOV-1994
PRIOR APPLICATION NUMBER: US 08/36,147
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
                                                                                                                                                                                                                  PRT;
                                 MOLECULE TYPE: protein
FENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                   Sequence 4, Application US/08581918A
                                                                                                                                                                                                                  STANDARD;
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                               121 EERGHRDVAGYLRTATGD 138
                                                                                                                                                                        120 EERGHRDVAGYLRTATGD 137
                                                          Query Match
Best Local Similarity 95.7%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
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US-08-581-918A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVWMMGSAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
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Patent No. 5994095
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUMTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 919; DB 3; Length 138 Pred. No. 5.92e-74; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 AA.
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: VIncent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELEPHONE: (617) 832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE 138 AA; 14722 MM; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/US95/0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Best Local Similarity 95.7%;
Matches 132; Conservative
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1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMMGSAR 60
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Patent No. 5801236
GENERAL INFORMATION:
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 919; DB 2; Length 138; Pred. No. 5.92e-74; 3; Mismatches 2; Indels
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COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
FILING DATE:
CLASSIFICATION 1435
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138
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JENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08480810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 138 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.7%;
Matches 132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-480-810-16
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Pred. No. 5.92e-74;
3; Mismatches 2; Indels 1; Gaps
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Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Mamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: AND THE OF T
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TVPE: amino acids
TVPE: amino acids
TVPE: amino acids
TVPE: ALLING MARE: INDEAL
TOPOLOGY: Illegar
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MOLECULE TYPE: protein
FENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08508735
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EERGHRDVAGYLRTATGD 138
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Best Local Similarity 95.7%;
Matches 132; Conservative
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US-08-508-735-16
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1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60
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Patent No. 5624819
GENERAL INFORMATION
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,106A
FILING DATE: 06-FEB-1994
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: FOX, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.050000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 AA.
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Pred. No. 5.92e-74;
3; Mismatches 2;
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MOLECULE TYPE: peptide
JENCE 138 AA; 14722 MW; 80871 CN;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.1%;
Best Local Similarity 95.7%;
Matches 132; Conservative
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COMPUTER READABLE FORM:
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                                                                   Washington
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                                                                                                                               USA
                                                                   CITY: Wash:
STATE: D.C
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US-08-474-177-16
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                                                                                                                         COUNTRY:
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Patent No. 6033847
GENERAL INFORMATION:
APPLICANT: Sherr Ph.D., Charles J.
APPLICANT: Blaral Ph.D., Hiroshi
APPLICANT: Hiral Ph.D., Hiroshi
APPLICANT: Okuda, Tsukasa
TITLE OF INVENTION: IRK4C-P18 and InK4d-P19, Inhibitors of
TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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Pred. No. 5.92e-74;
3; Mismatches 2; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,369
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION: NAME: 10 NAME: 10 NAME: 10 NAME: 10 NAME: NAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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FINCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25, Application US/08384106A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.7%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 EERGHRDVAGYLRTATGD 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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Sequence 16, Application US/08848251
Patent No. 5989815
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Cannon-Albright, Heward & Civiletti, LLP
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                         TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle TITLE OF INVENTION: Regulation NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 94.1%; Score 919; DB 2; Length 138; Best Local Similarity 95.7%; Pred. No. 5.92e-74; Matches 132; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 AA
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION UNMBER: GSI-001CP6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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JENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08848251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                   STREET: 60 Sta
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
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US-08-848-251-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 17-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: US 08/215,087
FILING DATE: US 08/215,086
FILING DATE: US 08/215,086
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/POCKET NUMBER: 28,957
RELEPHONE: 202-962-8300
INFORMATION FOR SEO ID NO: 16: SEQUENCE CHARACIERISTICS:
LENGTH: 138 amino acida
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FENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08627610
Patent No. 5919997
GENERAL INFORMATION:
APPLICANT: Beach, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08627610
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DePinho, Ronald A.
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US-08-627-610-4
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSIEL-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCES: 36
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Rashington
STATE: DC
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
CORPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/487,033
FILING DATE: 07-JUN-1995
FILING DATE: 17-MAR-1995
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTONEY/AGENT INFORMATION:
NUMBER: 18-MAR-1994
ANDENEY/AGENT INFORMATION:
NUMBER: 18-MAR-1994
ANDENEY/AGENT INFORMATION:
NUMBER: 18-MAR-1994
          Sequence 16, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 95.7%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 EERGHRDVAGYLRTATGD 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                           USA
                                                                                                                                                                         COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 VAELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVDAWGRLPVDLA 119
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                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
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                                                                                                                                                                 CLASSIETCATION:
CLASSIETCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
APPLICATION DATA: 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA: 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA: 18-MAR-1994
PRIOR APPLICATION DATA: 18-MAR-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
TELEPHONE: 202-962-4810
INFORMATION FOR SEG ID NO: '16:
SEQUENCE CHARACTERISTICS:
TEMEPRATION FOR SEG ID NO: '16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
TENCE 138 AA; 14722 MW; 80871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08487033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 138 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 EERGHRDVAGYLRTATGD 138
                                                       COMPUTER READABLE FORM:
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CITY: Washington
                USA
20005
                                                                                                                                                             FILING DATE
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                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMGSAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQVMMGSAR 59
                                                                                                                                                                                                                                                                                                                                                                                                    Score 919; DB 1; Length 138;
Pred. No. 5.92e-74;
3; Mismatches 2; Indels 1; Gaps
                                                REFERENCE/DOCKET NUMBER: 2484-109348-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
ENCE 138 AA; 14722 MW; 80871 CN;
NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                             TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Search completed: Thu Jul 20 08:40:18 2000 Job time : 8 secs.

121 XEXGHXDXXXYLRXAXGD 138 | | | | | | | | | | 120 EERGHRDVAGYLRTATGD 137

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:38:35 2000; MasPar time 10.90 Seconds 592.803 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-016-869A-4 (1-137) from USO9016869A.pep 977 1 MREBNKGMPSGGGSDEGLAT......LAEERGHRDVAGYLRTATGD 137 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

142080 segs, 47172406 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 42.515; Variance 86.121; scale 0.494 pir63 1:pir1 2:pir2 3:pir3 4:pir4 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

02	& Ouery Match	& Ouery Match Length	ğ	£	Description	Pred. No.
	3:		3			? ;
94.1		138	N	B55479	CDK4 inhibitor p14(IN	7.51e-158
76.7		130	N	178845	p15INK4b - mouse	3.56e-123
70.8		156	~	JE0141	cyclin dependent kina	1.22e-111
59.5		167	~	I58352	pl6INK4a - mouse	2.36e-89
33.7		164	~	A57378	cyclin-dependent kina	3.08e-40
32.2		166	~	A57379	CDK4/CDK6 inhibitor p	1.30e-37
31.9		166	~	B57378	cyclin-dependent kina	4.74e-37
29.1		41	~	I52720	gene pl5INK4B protein	7.40e-32
25.5		168	~	A55479		1.74e-25
25.3		168	7	B57379	CDK4/CDK6 inhibitor p	3.99e-25
14.3		1423	-	137275	death-associated prot	4.79e-07
14.3		1856	~	B35049	ankyrin 1, erythrocyt	4.79e-07
14.3	.,	1880	~	A35049	ankyrin 1, erythrocyt	4.79e-07
14.3	_	881	-	SJHUK .	ı,	4.79e-07
14.0	•	1848	N	S37771	ankyrin, erythrocyte	1.38e-06
0.	•	1862	~	149502	ankyrin – mouse	1.38e-06
13.6		2524	~	A35844	Xotch protein - Afric	5.56e-06
ĸ.	•	4377	~	A55575	ankyrin 3, long splic	7.86e-06
13.4		3924	~	S37431	ankyrin 2, neuronal l	1.11e-05
m.		2531	~	S18188	notch protein homolog	1.56e-05
13.2		1411	~	530355	alpha-latroinsectotox	2.20e-05
13.2		2318	~	S45306		2.20e-05
13.2	•	2555	(1	A40043	notch protein homolog	2.20e-05

		ALIGNMENTS						
1.03e-01	transcription factor	A35697	~	971	10.5	103	45	
-96	ankyrin - fruit fly (	139	7	1549	10.8	106	44	
•	/1 ym1	A34794	~	446	11.1	108	43	
2.19e-02	fnr-like t	S77600	~	249	11.1	108	42	
	probable ankyrin - sy	H71274	Н	934	11.3	110	41	
8.49e-03	G9a protein - human	S30385	N	1001	11.4	111	40	
3.25e-03	ankyrin-related unc-4	T15347	~	2039	11.7	114	39	
3.25e-03	ankyrin-related unc-4	T15344	~	1867	11.7	114	38	
3.25e-03		T15346	7	1815	11.7	114	37	
	ankyrin-related unc-4	T15345	~	1809	11.7	114	36	
•	ankyrin-related prote	A57282	N	1786	11.7	114	35	
2.35e-03	notch4 - mouse	T09059	ď	1964	11.8	115	34	
۳.	transcription factor	A53950	N	414	11.8	115	33	
₩.	notch protein - fruit	A24420	Н	2703	12.1	118	32	
Φ.	reg	B47169	N	323	12.1	118	31	
ď	hypothetical protein	T15888	~	209	12.4	121	30	
	SKD3 - mouse	I49045	~	677	12.5	122	29	
	cell-fate determining	A49128	~	2471	12.6	123	28	
1.68e-04	notch2 protein homolo	A56695	~	638	12.6	123	27	
8.58e-05	_	A46019	~	2531	12.8	125	56	
	notch3 protein - huma	S78549	~	2321	13.0	127	25	
3.10e-05	transmembrane protein	S42612	N	2437	13.1	128	24	

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Cloning and characterization of murine p16INK4a and p15INK4b
Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.;
Papadopoulos, N.; Markowitz, S.; Willson, J.K.; Kinzler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VAELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLA 120
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02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
28-Feb-1997
I78845
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#length 138  #molecular-weight 14722  #checksum 1236
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#length 130 - #molecular-weight 13788 #checksum 7879
                                                                                                                                                                                                                                             #gene GDB:CDKN2B; MTS2
##cross-references GDB:579577; OMIM:600431
#map_position 9p21-9p21
#map_cosition 9p21-9p21
KEYWORDS
cell cycle control; protein kinase inhibitor; tumor
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                                    K.W.; Vogelstein, B.
#journal Cancer Res. (1994) 54:6353-6358
#title Deletion of p16 and p15 genes in brain tumors.
#cross references WID:95079408
#accession I52713
                                                                                                                                           preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                           Length 138;
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##residues 1-130 ##label RES
##cross-references GB:S79252; NID:g1087092; PID:g1087093
                                                                                                                                                                                                                                                                                                                                                                                         Score 919; DB 2; Length 138 Pred. No. 7.51e-158; 3; Mismatches 2; Indels
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##cross-references GB:S75756; NID:g861470
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p15INK4b - mouse
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#accession I78845
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llarity 95.7%;
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#title A new regulatory motif in cell-cycle control causing specific
inhibition of cyclin D/CDK4.
#cross-references MUID:94081956
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Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.;
Johnson, B.E.; Skolnick, M.H.

#journal Science (1994) 264:436-440
#title A cell cycle regulator potentially involved in genesis of
many tumor types.

#cross-references MJID:94204645
                                                                                                                                                                                                                                                                                                                                                                                               Huang, C.; Deng, W.; Fu, J.
Chinese J. Biotechnol. (1997) 13:105-107
Molecular cloning and sequencing of P16 ink4 cDNA from hela
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This protein suppresses the function of cyclin DI/CDK4 and cyclin
                                                                                                                                                                                                                                                                                            Huang, C.G.; Deng, W.; Fu, J.L.
Chinese J. Biotechnol. (1997) 13:105-107
Molecular cloning and sequencing of Pl6ink4 cDNA from hela
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this sequence has been corrected in reference I59268
                                                                                                  JE0141 #type complete
cyclin dependent kinase - human
cyclin dependent kinase - human
cDM4 inhibitor 2A; multiple tumor suppressor 1 (MTS1)
#formal_name Homo sapiens #common_name man
02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change
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##cross-references GDB:335362; GDB:CDKN2A; OMIM:600160
#map_position 9p21-9p21
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JE0141
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##residues 51-152 ##label RE2
##cross-references GB:S69804; NID:9546272
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#cross-references MUID:95257949
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# yournal Mol. Cell. Biol. (1995) 15:2682-2688
#title Identification of human and mouse pl9, a novel CDK4 and CDK6
#cross-references MUID:95257949
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Cloning and characterization of murine p16INK4a and p15INK4b
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C.; Beach, D.; Sherr,
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                                                                                                                                                                                                  77 ATLIRPVHDAAREGFLDTLVVLHRAGARLDVRDAMGRLPVDLAEERGHRDVAGYLRTATG 136
                                                                                                                                            18 LAITPA-RGLVEKVRHSWEAGADPHGVNRFGRRAIQVWMGSARVAELLLLHGAEPNCADP 76
                                                                                                                           16 LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADP 75
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#formal_name Mus sp. #common_name mouse
26.Jul-11996 #sequence_revision 26.Jul-1996 #text_change
28-Feb-1997
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 #superfamily unassigned ankyrin repeat proteins
cell cycle control; protein kinase inhibitor; tumor
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                                                                    Score 692; DB 2; Length 156
Pred. No. 1.22e-111;
6; Mismatches 10; Indels
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Pred. No. 2.36e-89;
20; Mismatches 22;
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#length 167 #molecular-we1ght 17870
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Trono, D.; Richter, K.H.; Walker,
                                                                                                                                                                                                                                                                           #type complete
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                                                                    Query Match 70.8%;
Best Local Similarity 85.8%;
Matches 103; Conservative
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Best Local Similarity 65.6%;
Matches 80; Conservative
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Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A. Mol. Cell. Biol. (1995) 15:2682-2688
Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to pl6(ink4).
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#title Novel INK4 proteins, pl9 and pl8, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.
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                                                                                         #superfamily unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology #length 164 #molecular-weight 17362 #checksum 5271
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                                                                                                                                                                                                                                                                                                             A57379 #type complete CDE4/CDE6 Inhibitor pl9 - mouse #formal_name Mus musculus #common_name house mouse 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
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                                                                                                                                                                                      Score 329; DB 2; 1
Pred. No. 3.08e-40;
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-164 ##label
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#length 166 #mol
                   ##cross-references GB:U20498
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Best Local Similarity 46.6%;
Matches 55; Conservative
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Association of rat p15/IKK4b/p161XR4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal
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CDK6 inhibitor pl8 - human
cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent
kinase CDK6 inhibitor pl8
#formal_name Homo sapiens #common_name man
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
                                                                          #Fresidues 1-166 ##label CHA 1
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O'Keefe, C.L.; Matera, A.G.; Xiong, Y.
fjournal Genes Dev. (1994) 8:2839-2952
#title Growth suppression by pl8, a p16(INK4/MTS1)- and p14
(INK4B/MTS2)-related CDK6 inhibitor, correlates with wild-type pRb function.
#cross-references MUID:95095079
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#formal_name Rattus sp. #common_name rat
26-Jnl-1996 #sequence_revision 26-Jul-1996 #text_change
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Pred. No. 4.74e-37;
20; Mismatches 38; Indels
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Pred. No. 7.40e-32;
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                     **status preliminary
##molecule_type mRNA
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Best Local Similarity 97.6%;
Matches 40; Conservative
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Best Local Similarity 47.4%;
Matches 54; Conservative
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##molecule_type mRNA
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#journal Mol. Cell. Biol. (1995) 15:2672-2681
#title Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.
#cross-references MUID:95257948
#accession B57379
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##readlucs 1-168 ##label HIR
##readlucs 1-168 ##label HIR
##cross-references GB:U19596; NID:9790566; PIDN:AAC52193.1; PID:9790567
FFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
DS cell cycle control
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##residues 1-168 ##label GUA
##cross-references GB:U17074; NID:g639713; PIDN:AAC50074.1; PID:g639714
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#map_position 1p32-1p32
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin repeat proteins; ankyrin repeat cela cycle control; protein kinase inhibitor; tumor
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death-associated protein kinase (EC 2.7.1.-) - human
calmodulin-dependent protein kinase homolog; DAP kinase
#formal_name Homo saptens #common_name man
16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B57379 #type complete CDK4/CDK6 inhibitor pl8 - mouse fformal_name Mus musculus #common_name house mouse 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 KDRIGFA-VIHDAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 ADPAILTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYL 131
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#length 168  #molecular-weight 18127  #checksum 9379
                                                                                                                                                                                                                                                                                                                                                              Length 168;
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                                                                                                                                                                                                                                                                                                                                                              Score 249; DB 2; Length 168
Pred. No. 1.74e-25;
28; Mismatches 43; Indels
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Local Similarity 39.0%;
les 46; Conservative
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Best Local Similarity 38.2%;
Matches 47; Conservative
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B57379
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ALTERNATE_NAMES
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370-402
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436-468
469-501
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733-765
766-798
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REFERENCE
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2-1856
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                                                                                                        and a novel
                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis
activity is calmodulin dependent
#superfamily death-associated protein kinase; ankyrin repeat
homology; protein kinase homology
apoptosis; ATP; calmodulin binding; phosphotransferase;
serine/threonine-specific protein kinase; tandem repeat
                   A55614
Deiss, L.P.; Feinstein, E.; Berissi, H.; Cohen, O.; Kimchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain protein kinase homology #label KINN
#region protein kinase ATP-binding motif\
#region calmodulin binding #status predicted\
#domain ankyrin repeat homology #label ANI\
#active_site Lys\, Glu, Asp\, Lys #status predicted
#length 1423 #molecular-weight 159161 #checksum 6280
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ankyrin 1, erythrocyte splice form 3 - human

ankyrin 2.1, erythrocyte; ankyrin-R

ankyrin 2.2, erythrocyte;

#formal_name Homo sapiens #common_name man
17.Nov-1995 #sequence_revision 17-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                        catalyzes the formation of peptidyl-serine-phosphate peptidyl-threonine-phosphate using ATP
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                                                                              #journal Genes Dev. (1995) 9:15-30
#title Identification of a novel serine/threonine kinase 15-kD protein as potential mediators of the gamm interferon-induced cell death.
#cross-references MUID:95129831
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                                                                                                                                                                                                                           ##residues 1-1423 ##label RES
##cross-references EMBL:X76104; NID:9434846; PID:9434847
                                                                                                                                                                                                                                                                1-1856 ##label LAM
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  137275; S39269
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##residues 1-18
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470-502
503-568
536-568
569-601
602-634
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CLASSIFICATION
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403-435
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*product ankyrin 1, erythrocyte form 3 *status predicted
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#product ankyrin 2.2, erythrocyte #status predicted
#label MA2\
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ankyrin 1, erythrocyte splice form 2 - human
ankyrin 2.1, erythrocyte; ankyrin-R
ankyrin 2.2, erythrocyte;
ankyrin 2.2, erythrocyte
ankyrin 2.2, erythrocyte
2.7-in-1990 #sequence_revision 01-0ct-1992 #text_change
04-Sep-1998
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#domain ankyrin repeat homology #label AN23
th 1856 #molecular-weight 203445 #checksum 6521
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Pred. No. 4.79e-07;
25; Mismatches 55; Indels 8;
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AN05/
AN06/
AN07/
#gene GDB:ANK1; ANK
##cross-references GDB:118737; OMIM:182900
#map_position 8911.2-8911.2
CLASSIFICATION #911.2-8p11.2
ALEXWORDS alternative splicing
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##cross-references GB:M28880
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#length 1856 #molecu
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Best Local Similarity 32.3%;
Matches 42; Conservative
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A35049
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A33219
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828-1382
1383-1881
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#journal
#title
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2-827
44-76
110-1143-171
112-204
205-237
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535-567
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#journal Nature (1990) 344:36-42
#title Analysis of CDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle control proteins.
#accession $808.75
##molecule_type mRNA
##residues
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#product ankyrin 2.2, erythrocyte #status predicted
#label MA2\
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#molecular-weight 206066 #checksum 6968
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AN06\
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                                                         ##cross-references GDB:118737; OMIM:182900
#mep_position 8pli.2-8pli.2
#smp_position 8pli.2-8pli.3
KEYNORDS #superfamily ankyrin; ankyrin repeat homology
KEYNORDS alternative splicing; cytoskeleton
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119 AEERGHRDVA 128
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Hermann, J.; Barel, M.; Frade, R.
Blochem. Blophys. Res. Commun. (1994) 204:453-460
Human erythrocyte ankyrin, a cytoskeleton component,
generates the p57 membrane proteinase which cleaves C3, the
third component of complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Davis, L.H.; Bennett, V.
#journal J. Biol. Chem. (1990) 265:10589-10596
#title Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger and spectrin.
#cross-references MUD:90285190
#accession A35443
##molecule_type protein
##molecule_type protein
##residues

'L',802-814;862-863,'X',419-422,'H',424,'LQ';797-800,
"L',802-814;862-863,'X',911-912 ##label DAV
protein
2-7, %x, 917, %x, 19-20, °T', 22-30;733-749, AA',751-753;
828-833, %x, 835-855, °K',857-869, °XX, 862-871,959-1003;
1106-1120, °XX, 1123-1128;1149-1172;1282-1285, °E',
1287-1288,1307-1332,1345-1365, %x, 1367;1383-1427;
1601-1630,16166-1698, °D', 1700;1763-1772 ##label LUX
845-Arg and 1392-Thr were also found
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Pred. No. 4.79e-07;
25; Mismatches 55; Indels
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Best Local Similarity 32.3%;
Matches 42; Conservative
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Birkenmeler, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.;
Lux, S.E.; Barker, J.E.
J. Biol. Chem. (1993) 268:9533-9540
Complex patterns of sequence variation and multiple 5' and 3'
ends are found among transcripts of the erythroid ankyrin
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                                                               552 AELLLERDAHPNAAGKNGLT-PLHVAVHHNNLDIVKLLLPRGGSP-HSP-AWNGYTPLHI 608
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14.0%; Score 137; DB 2; Length 1848;
Best Local Similarity 33.9%; Pred. No. 1.38e-06;
Matches 39; Conservative 21; Mismatches 48; Indels 7; Gaps
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#molecular-weight 202576 #checksum 2542
193 NANPNLATTAG-HTPLHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAKYGKVRV
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#accession S37771
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##residues
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Search completed: Thu Jul 20 08:38:48 2000 Job time: 13 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp Run on:

Thu Jul 20 08:39:06 2000; MasPar time 6.93 Seconds 602.124 Million cell updates/sec Tabular output not generated.

>US-09-016-869A-4
(1-137) from USO9016869A.pep
977
1 MREENKGMPSGGGGDEGLAT.....LAEERGHRDVAGYLRTATGD 137 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

83857 seqs, 30454973 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot38 1:swissprot

Mean 43.541; Variance 77.735; scale 0.560 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Query Match Length DB
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76.9 130 1
76.7 130 1
70.8 156 1
59.5 167 1
58.5 171 1
33.7 166 1
32.2 166 1
25.5 168 1
25.3 168 1
14.3 1431 1
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118	115	108	108	103	103	102	100	100	66	86	86	86	86	86	97	97	97	97	97	26	96
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	0.4	41	42	43	44	45

#### ALIGNMENTS

ST			RR SEQUENCE FROM N.A.  RX MEDLINE; 94359613.  RA Hannon G.J., Beach D.;  RT "PISINK4B is a potential effector of TGF-beta-induced cell cycle RT arrest.";  R Nature 371:257-261(1994).  RN SEQUENCE OF 53-138 FROM N.A.  RX MEDLINE; 94204645.  RA Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,  RA Tavidjana S.V., Stockert E., Day R.S. III, Johnson B.E.,  RA Skolnick M.H.;	"A cell cycle regulator potentially in types."; Science 264:436-440(1994). [4] VARIANTS LUNG ADENOCARCINOMA GLU-47 AN MEDLINE; 95188190. Okamoto A., Hussain S.P., Hagiwara K., Demetrick D.J., Serrano M., Hannon G.J. Xiong Y., Beach D.H., Yokota J., Harrian G.J.	RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in RT primary and metastatic lung cancer."; R Cancer Res. 55:1448-1451(1955). CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.	
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55:1607-1612(1995)
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilenserial.
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                           DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
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*Association of rat pl5INK4B/pl6INK4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal tumors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y., Tsuchiya H., Kikuchi Y., Mitani H.; *Molecular genetic basis of renal carcinogenesis in the Eker rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; ANK repeat; Disease mutation. 2 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G -> E (IN LUNG ADENOCARCINOMA).

/FIId-VAR_001488.

A -> V (IN LUNG ADENOCARCINOMA).

/FIId-VAR_001489.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 919; DB 1; Length 138;
Pred. No. 7.32e-179;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SA -> TP (IN REF. 2).
MISSING (IN REF. 2).
QLL -> HSW (IN REF. 2).
OD6FFBDFA6FEAD21 CRC64;
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SUBUNIT: HETERODIMER OF P14 WITH CDK4
                                                                                                                SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    model of tuberous sclerosis (Tsc2)."; Mol. Carcinog. 14:23-27(1995).
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23 M
34 0
14722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U17075; AAC50075.1; -. EMBL; L36644; AAA50282.1; -. EMBL; S69805; AAD14049.1; -. MIM; 600411; -. Cell cycle; Anti-oncogene; Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 46-86 FROM N.A. MEDLINE; 95228036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 EERGHRDVAGYLRTATGD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EERGHRDVAGYLRTATGD 137
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Best Local Similarity 95.7%;
Matches 132; Conservative
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103
47
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23
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138 AA;
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CDN5_RAT
P55272;
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SEQUENCE
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                                                      SIMILARITY).
--- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
--- SUBUNIT: HETERODICTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
--- INITIATION CODONS IN THE SAME READING FRAME.
--- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
--- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
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Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
"Cloning and characterization of murine pl6INK4a and pl5INK4b genes.";
Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CHAIN 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 EPNCADPATLTRPVHDAAREGFLDTLMVLHKAGARLDVCDAWGRLPVDLAEEQGHRDIAR 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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01-OCT-1996 (Rel. 34, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 130;
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Pred. No. 4.85e-140;
11; Mismatches 7; Indels
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2 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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M.
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95
13748 1
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Best Local Similarity 85.2%;
Matches 109; Conservative
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PFAM; PF00023; ank;
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95380169.
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|130 YLRTATGD 137
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MEDLINE: 94338359.
Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41
(cyclin-dependent kinase-4 inhibitor) gene in human primary non-small cell lung carcinomas.";
Biochem. Biophys. Res. Commun. 202:1426-1430(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hussussian C.J., Struewing J.P., Goldstein A.M., Higgins P.A.T., Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.; "Germline pl6 mutations in familial melanoma.";
                                                                                                                  "A cell cycle regulator potentially involved in genesis of many tumor types.";
                                                                                                                                                                                                                                                                                                                                                                                                                              Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.; "Structural basis for inhibition of the cyclin-dependent kinase Cdk6 by the tumour suppressor pl6INK4a."; Nature 395:237-243(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okamoto, A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R., Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M., Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.; "Mutations in the pifink4/mz1/CDKN2, pl5ink4B/mr52, and pl8 genes Primary and metastatic lung cancer."; cancer Res. 55:1448-1451(1995).
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                                                                                                                                                                                                                                                                   Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.; "Requisition of pl6CDKN2 expression and its implications for cell immortalization and senescence."; MOI. Cell. Biol. 16:859-867(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The MTS1 gene is frequently mutated in primary human esophageal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144. MEDLINE; 95060835.
Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 96121580.
Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M., Haluska F.G., Dracopoll N.C., Hayward N.K., Fountain J.W.; "Mutations of the CDKN2/pl6INK4 gene in Australian melanoma kindreds.";
                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6
                                                 Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshma.
Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith-Soerensen B., Hovig E.; "CDKN2A (pl6INK4A) somatic and germline mutations."; Hum. Mutat. 7:294-303(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96377761.
Dracopoli N.C., Fountain J.W.;
"CDKN2 mutations in melanoma.";
cancer Surv. 26:115-132(1996).
OF 51-152 FROM N.A. 94204645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVIEW ON MELANOMA VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogene 9:3737-3741(1994).
                                                                                                                                                                       Science 264:436-440(1994).
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                                                                                                                                                                                                                    SEQUENCE OF 1-20 FROM N.A.
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MEDLINE; 96303699.
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                                                                                                 Skolnick M.H.;
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                      MEDLINE;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@15b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ĥ
                                                                                                                                                                                                                                                                 -i- SUBUNIT: HÉTERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
-i- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
-i- INDUCTION: BY TGF-BETA.
-i- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
STRAIN-C57BL/6J X DBA;
MEDLINE; 9732242.
MEDLINE; 9732242.
MELUBYES; 9732242.
MELUBYES M., de Castro I., Santos J., Melendez B., Mangues R., Serrano M., Pellicer A., Fernandez-Piqueras J.;
Finactivation of the cyclin-dependent Kinase inhibitor pi5INK4b by deletion and de novo methylation with independence of pi6INK4a alterations in murine primary T-cell lymphomas.";
Oncogene 14:1361-1370(1997).
-I-FUNCTION: INTERACTS STRONGLY WITH CDM4 AND CDM6, POTENT INHIBITOR.
POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 EPNCADPALLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAWGRLPVDLAEEQGHRDIAR 122
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P42771; 015191;
01-NOY-1995 (Rel. 32, Created)
15-JUL-1999 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4A)
CDKNIR-IPLE TUMOR SUPPRESSOR 1) (MILIPLE TUMOR SUPPRESSOR 1) (MIS1).
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"A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D/CDK4.";
Nature 366:704-707(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 130;
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ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
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Pred. No. 1.40e-139;
11; Mismatches 7;
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EMBL; U66084; AAB39833.1; JOINED.
MGD; MG1:104737; CDKN2B.
THE PF00023; ABF 3. 3. Cell cycle; Anti-oncogene; Repeat; ANK repeat.
                                                                                                                                                                                                                                                                                                                                                                INHIBITORS.
-1- SIMILARITY: CONTAINS 2 ANK REPEATS.
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Best Local Similarity 85.2%;
Matches 109; Conservative
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US-09-016-869A-4.rsp

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Query Match
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DORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORRANDORR
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                                                                      CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILNE; 9632329.

FILZGERAID MEDILNE; 9632329.

FILZGERAID M.C., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,
Isselbacher K.J., Sober A.J., Haber D.A.;
Prevalence of germ-line mutations in pi6, pl9ARF, and CDK4 in
Familial melanoma: analysis of a clinic-based population.";
Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).
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MEDILIE; 98087572.
Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
"Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone families in France.";
Families in France.";
Hum. Mol. Genet. 7:209-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97472457.

MINIOR M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K., Frischauf A.-M., Batalle V., Peters G., Cuzick J., Selby P., Bishop D.T., Bishop J.N.,

"Germline mutations of the CDKN2 gene in UK melanoma families.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variant Pancrearic Carcinoma CYS-146.
Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,
Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;
"Novel germline ploink allele (Aspl45cys) in a family with multiple pancreatic carcinomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glioma and carcinoma of the pancreas.";

Hum. Mutat. 12:121-211(1998).

-!- FUNCITON: INTERACIS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS
ABILITY TO INTERACI WITH CYCLINS D. COULD ACT AS A NEGATIVE
REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.
-!- SUBUNIT: HETERODIMER WITH CDK4 OF CDK6.
-!- DISEASE: CDKNZA MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.
MEDLINE; 97472457.
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Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
Hum. Mol. Genet. 7:941-941(1998).
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Gretarsdottir S., Olafsdottir G.H., Borg A.;
Five novel somatic CDKN2/p16 mutations identified in melanoma,
                                                                                                                            Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,
Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach
Dracopoli N.C.;
                                                                                                                                                                                                                                                                          "Mutations associated with familial melanoma impair p16INK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHIBITORS.
-1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mol. Genet. 6:2061-2067(1997).
Mol. Genet. 4:1845-1852(1995).
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EMBL; L27211; AAA92554.1; -. EMBL; U12820; AAB60645.1; -.

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/FIId=VAR_001409.

A -> P (IN A LUNG TUMOR AND MELANOMA).

/FIId=VAR_001410.

A -> S (IN A BILIARY TRACT TUMOR).

/FIId=VAR_001411.

G -> D (IN A PANCREAS TUMOR).

/FIId=VAR_001412.

R -> C (IN MELANOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
CCCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                  /FIId-vAR_001408.
L -> P (IN A BILIARY TRACT TUMOR AND A FAMILIAL MELANOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                     Repeat; ANK repeat; Disease mutation;
                                                                                                                    ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 3.
ANK MOTIF 4.
D -> E (IN A BILIARY TRACT TUMOR).
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E -> D (IN A BILLARY TRACT TUMOR).

fTId-VAR_001415.

L -> P (IN FAMILIAL MELANOMA).

/FIId-VAR_001416.

E -> D (IN A BILLARY TRACT TUMOR).
                                                                                                                                                                                                                                                                                                                    /FIId=VAR_001413.
R -> P (IN FAMILIAL MELANOMA AND
MELANOMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 692; DB 1; Length 156
Pred. No. 1.62e-126;
6; Mismatches 10; Indels
                                                                                                            4 X ANK MOTIF REPEATS
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            JOINED.
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larity 85.8%;
Conservative
EMBL; U12818; AAB60645.1; JC
EMBL; U18819; AAB60645.1; JC
EMBL; S69804; AAD14048.1; --
EMBL; X94154; CAA63870.1; --
PDB; 1B17; 16-FEB-99.
MIM; 600160; --
                                                                                    Cell cycle; Anti-oncogene;
Polymorphism; 3D-structure.
DOMAIN 12 141
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                                                          MIM; 600160; -.
PFAM; PF00023; ank; 3.
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nes 103; Conser
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127
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CDN2_MOUSE
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TISSUE-THYMUS
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                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; ANK repeat; Alternative initiation.
4 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECTION STATEMENT OF STATEMENT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KIRASE 4 INHIBITOR A (CDK4I) (P16-INK4A)
(TUMOR SUPPRESSOR CDKN2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SAADRLARAAQGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHVAALLLNYGADSN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN SHORT ISOFORM).
88C4588A105ECB8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.75e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 AA.
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-1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                   INHIBITORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 AA; 17870 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L76150; AAA85453.1; -.
MGD; MGI:104738; CDKN2A.
PFAM; PF00023; ank; 2.
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65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell cycle; Anti-oncogene;
DOMAIN 4 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80; Conservative
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101
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15-JUL-1999
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CDN2_MONDO
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VARSPLIC
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셤
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                                                                                                                                                                                                                   EMBL; AF064808; AAC2369.1; -.

EMBL; AF064808; AAC23670.1; -.

EMBL; AF064808; AAC23670.1; -.

Cell cycle; Anti-oncogene; Repeat; Alternative initiation.

DOMAIN

46 77 ANK MOTIF I (INCOMPLETE).

REPEAT 46 77 ANK MOTIF 2.

REPEAT 111 143 ANK MOTIF 2.

REPEAT 111 143 ANK MOTIF 3.

REPEAT 14 169 ANK MOTIF 4.

VARSPLIC 1 34 MISSING (IN SORT ISOFORM).

SEQUENCE 171 AA; 18707 MM; 694264F5DOF4F6CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 SGEKLTEAAARGRIEVVTELLELGTNPNAVNRFGRSAIQVMMMGNVRLAAILLQYGAEPN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 TPDPTILITEPVHDAAREGFILDTIMLIHRAGARLDVRDSWGRLPVDLAEEQGHHLVVAYLR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 SDEGLA-TPARGLVEKVRHSWEAGADPNGVNRFGRRAIQVWMGSARVAELLLLHGAEPN 72
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"Molecular cloning, expression pattern, and chromosomal localization of human CDKNZD/INK4d, an inhibitor of cyclin D-dependent Kinases."; Genomics 29:623-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96362662.

Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,
Zariwala M., Matera A.G., Xlong Y.;
"Isolation and characterization of p19INK4d, a p16-related inhibitor
specific to CDK6 and CDK4.";
Mol. Biol. Cell 7:57-70(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEGUENCE FROM N.A.
Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,
Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mutation testing in melanoma families: INK4A, CDK4 and INK4D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.; "Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to p16ink4."; Moi. Cell. Biol. 15:2682-2688(1995).
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 572; DB 1; Length 171;
Pred. No. 2.96e-99;
17; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDN7_HUMAN STANDARD; PRT; 166 AA.
P55273; Q13102;
Q1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.5%;
llarity 69.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE; 96121373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 83; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                  "Structure of the cyclin-dependent kinase inhibitor pl9Ink4d.";
Nature 389:999-1003(1997).
Nature 389:999-1003(1997).
-i - FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
-i - SIMILARITY: BELONGS TO THE CDKN2 PAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 GARARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPNVQDAS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hiral H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.; "Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
KINASE 4 INHIBITOR C) (P18-INK4C).
CDKN2C OR CDKN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 G-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luh F.X., Archer S.J., Domaille P.J., Smith B.O., Owen D., Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
                                                                                                                                                                          Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.; "Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to p16ink4."; Mol. Cell. Biol. 15:2682-2688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 315; DB 1; Length 166;
Pred. No. 9.05e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Mismatches 38; Indels
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9E74F5C23B7EBCB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 1.
ANK MOTIF 3.
ANK MOTIF 4.
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                                                                                                    Mol. Cell. Biol. 15:2672-2681(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 AA; 17894 MW;
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DOMAIN 7 137
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MGD; MGI:105387; CDKN2D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
72
104
137
137
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STRAIN-C57BL KAPLAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                   MEDLINE; 95257948.
                                                                                                                                                               95257949.
                                                                                                                         [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          MEDLINE; 98013176.
                                                                                                                                                                                                                                                                   [3]
STRUCTURE BY NMR.
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                                                                                                                                                                                                                                                                                                                                                                   Laue E.D.;
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                                                                                                                                                                 MEDLINE;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                          Holak T.A.;

"Structure of human cyclin-dependent kinase inhibitor p19(INK4d):
"Structure of human mkyrin-repeat-containing structures and
implications for the dysfunction of tumor suppressor p16(INK4a).";
Structure 6:1279-1290(1998).

-I - FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
-- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                   MEDLINE; 98455510.
Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engh R.A.,
                                                                          Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.; "Structural basis for inhibition of the cyclin-dependent kinase Cdk6 by the tumour suppressor pl6INK4a."; Nature 395:237-243(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 ATPARGLVEKVRHSWEAG-ADPNGVNRFGRRAIQVMMGSARVAELLLLHGAEPNCADPA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 GAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSTAIALELLKQGASPNVQDTS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 G-TSPVHDAARTGFLDTLKVLVEHGADVNVPDGTGALPIHLAVQEGHTAVVSFLAAES 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
7
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; ANK repeat; 3D-structure.
4 X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 2.
ANK MOTIF 4.
                                      RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Indels
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> P (IN REF. 3).
2FACD11CF56340DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDN7_MOUSE STANDARD; PRT; 166 AA. 060773; 060794; 010-100-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 329; DB 1; I
Pred. No. 9.77e-46;
23; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                        INHIBITORS.
                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U49399, AAB03772.1; -. EMBL, U40343, AAB18139.1; -. EMBL, U20498, AAAB436.1; -. EMBL, AF061327; AAC27450.1; -. PDB; 1BD8; 16-FEB-99. PDB; 1BD8; 14-OCT-98. MIM; 600927; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 46.00,
55, Conservative
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105
159
166 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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2; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Growth suppression by p18, a p161NK4/MTS1- and p141NK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb function."; Genes Dev. 8:2939-2952(1994).
                                                                                                                                                                                                                                                                                                                                                        Venkatazemani R., Swaminathan K., Marmorstein R.;
"Crystal structure of the CDK4/6 inhibitory protein pl81NK4c provides
insights into ankyrin-like repeat structure/function and
tumor-derived pi61NK4 mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 99175088.
Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Maille P., Selby T.,
gaal M.-D.;
                                                                                                                                                              Blais A., Labrie Y., Poullot F., Lachance Y., Labrie C.;
Structure of the gene encoding the human cyclin-dependent kinase
inhibitor pl8 and mutational analysis in breast cancer.";
Biochem. Biophys. Res. Commun. 247:146-153(1998).
          SEQUENCE FROM N.A.
MEDLINE; 95095079.
Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat; Disease mutation; 3D-structure.
                                                                                                                                                                                                                                                           Lapointe J., Lachance Y., Labrie Y., Labrie C.; A pl8 mutant defective in CDK6 binding in human breast cancer
                                                                                                                       SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INHIBITORS.
                                                                                                                                                                                                                                                                                                                    [4]
X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF041248; AAC39782.1; -.
EMBL; AF041250; AAC39783.1; -.
EMBL; AF041249; AAC39783.1; JOINED.
PDB; 1IHB; 13-JAN-99.
PDB; 1BU9; PRELIMINARY.
MIM; 603369; -.
                                                                                                                                                                                                                                                                                                     Cancer Res. 56:4586-4589(1996).
                                                                                                                                                                                                                                  VARIANT BREAST CANCER PRO-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MINI COCCIS, ank; 3.
Cell Cycle; Repeat; ANK re
DOMAIN 5 135
REPEAT 5 36
REPEAT 69 101
REPEAT 69 101
REPEAT 102 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U17074; AAC50074.1;
                                                  Matera G.A., Xiong Y.;
                                                                                                                                                                                                                                               MEDLINE; 96438606.
                                                                                                                                              MEDLINE; 98300299.
                                                                                                                                                                                                                                                                                                                                                MEDLINE; 98100086.
                                                                                                                                                                                                                                                                                                                                                                                                                                [5]
STRUCTURE BY NMR
                                                                                                                                     TISSUE-BREAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HITAI H., Roussel M.F., Rato J.-Y., Ashmun R.A., Sherr C.J.;
"Novel INK4 proteins, p19 and p18, are specific inhibitors of the
cyclin D-dependent kinnases CDK4 and CDK6.";
MOI. Cell. B101. 15:2672-2681(1995).
-I- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
CELL GROWTH AND PROLIERRATION WITH A CORRELATED DEPENDENCE ON
ENDOGRNOUS RETINDBLASTOMA PROTEIN RB.
-I- SUBUNIT: HETERODIMER OF P18 WITH CDK6 (BY SIMILARITY).
-I- SUBUNIT: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                          6 GNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPDL 65
                                                                                                                                                            6 GNELASAAARGDLEQLISLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPNL 65
                                                                                                             1; Gaps
                                                                                                                                                                                                       66 KDRIGFA-VIHDAARAGFLDILQILLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
A -> P (IN BREAST CANCER; LOSS OF CDK6
                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPERNDENT KINASE 6 INHIBITOR (PI8-INK6) (CYCLIN-DEPENDENT
KINASE 4 INHIBITOR C) (PI8-INK4C).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 247; DB 1; Length 168; Pred. No. 1.11e-28;
                                                                            Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Mismatches 46; Indels
                                                                                                             43; Indels
                            /FTId-VAR_001490.
5D66AFA715186E9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC88D5489307E128 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 4.
                                                                            Score 249; DB 1;
Pred. No. 4.38e-29;
                                                                                                           28; Mismatches
                                                                                                                                                                                                                                                                                                    168 AA
                  INTERACTION)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell cycle; Repeat; ANK repeat.

DOMAIN 5 135 4 X

REPEAT 5 36 ANK

REPEAT 37 68 ANK

REPEAT 69 101 ANK

REPEAT 102 135 ANK
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36 AN
68 AN
101 AN
135 AN
                                              18127 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.3%;
38.2%;
                                                                            Similarity 39.0%; 46; Conservative
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les 47; Conservative
                                                                                                                                                                                                                                                                                                    STANDARD;
72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL KAPLAN;
MEDLINE; 95257948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 AA;
                                               ¥.
                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
72
                                              168
                                                                                                                                                                                                                                                                                                  CDN6_MOUSE
Q60772;
                                              SEQUENCE
                                                                            Query Match
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                   CDKN2C
                                                                                                             Matches
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        # Transferase; Serine-Chreonine-Protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.

Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.

DOMAIN 13 26 PROTEIN RINASE.

BINDING 42 42 ATP (BY SIMILARITY).

ACT_SITE 139 139 BY SIMILARITY).

ACT_SITE 139 139 BY SIMILARITY).

DOMAIN 373 405 ANK MOTIF 1.

REPEAT 373 405 ANK MOTIF 2.

REPEAT 473 505 ANK MOTIF 2.

REPEAT 473 505 ANK MOTIF 4.

REPEAT 506 538 ANK MOTIF 6.

REPEAT 570 604 ANK MOTIF 6.

REPEAT 572 604 ANK MOTIF 6.
             66 KDGTGFA-VIHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKEGHLPVVEFLMK 124
                                                                                                                                                                                                                                                               Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.; "Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell
                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES.
                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DEATH-ASSOCIATED PROTEIN KINASE I (EC 2.7.1.-) (DAP KINASE 1).
                                                                                                                                                                                 DAPKI OR DAPK.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                               PRT; 1431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 8 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X76104; CAA53712.1; -. HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                           PIM: AUTOPHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00023; ank; 8.
PFAM; PF00069; pkinase; 1.
PFAM; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                            Genes Dev. 9:15-30(1995).
                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 164-171.
Feinstein E.;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      MEDLINE; 95129831.
                                            125 HTA 127
                                                                 134 ATG 136
                                                                                                   LT 11
DAPK_HUMAN
P53355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 600831
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                                                                                                                                                                                                                                                  517 LTASARGYHDIVECLAEHGADLNACDKDGHIALHLAVRRCQMEVIKTLLSQGCFVDYQDR 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet. 13:214-218(1996).

Nat. Genet. 13:214-218(1996).

- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL ELEMENTS: BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN GP85, AND TO THE CYTOSKELETAL PROTEINS FORDER. TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE CYTOSKELETAL PROTEINS FORDER. TOBULIN. VIKENITIN AND DESMIN. ERYTHROCYTE ANKRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASHIC DOMAIN OF THE EXTTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
                                                                                                                                                                                                                                                                                         Lux S.E., John K.M., Bennett V.; "Analysis of CDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- PTM: REGULATED BY PHOSPHORYLATION.
-1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
-1- DISEASE: DEFECTS IN ANKI ARE THE CAUSE OF DOMINANT AND RECESSIVE HEREDITARY SPHEROCYTOSIS (HS).
-1- SIMILARITY: CONTAINS 24 ANK REPEATS.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96225450.

Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.,
"Ankyrin-1 mutations are a major cause of dominant and recessive
                                                                                                                                                                                                                                                                                                                                                                         577 HGNT-PLHVACKDGNMPIVVALCEANCNLDISNKYGRTPLHLAANNGILDVVRYL 630
                                                                                                                                                                                                                                                                                                                                                                                                                77 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYL 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher Chenng M.C., Kan Y.W., Palek J.; "cohns sequence for human styrin."; Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
                                                                                                                    Score 140; DB 1; Length 1431;
Pred. No. 2.39e-08;
23; Mismatches 53; Indels
                         K->A: LOSS OF ACTIVITY.
MW; 9EE84811004A155B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
11-FEB-2000 (Rel. 39, Last annotation update)
ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
IISSUE-HEMATOPOIETIC;
MEDLINE; 90158830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebra
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1880 AA
DEATH DOMAIN.
                             42
160017 1
                                                                                                                          14.38;
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 344:36-42(1990).
1397
                                                      1431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLASMA MEMBRANE
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                                                                                                                                                       Local Similarity
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MEDLINE; 90175370.
1313
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P16157;
                                MUTAGEN
SEQUENCE
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN ISOFORM 2.2).
H -> D (IN ISOFORM 2.2).
TVEGPLEDPSELEVDIDIFMKHSKDHTSTPNP -> ELRGS
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ISOFORM).
                                                                                                                                                                                                                                                                                                                            DOMAIN).

55 KD REGULATES
THE BINDING OF ANKIRIN TO SPECTRIN
AND THE BAND 3 PROFEIN).
24 X ANK MOTIF CINCOMPLETE).
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PFAM; PF00023; ank; 22.
PFAM; PF00791; 205.1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
Phosphorylation; Lipoprotein; Multigene family; Disease mutation;
Eliliptocytosis; Polymorphism.
                                                                                                                                                                                                                                                                                     KD DOMAIN (ANION EXCHANGE PROTEIN
                                                                                                                                                                                                                                                                                     89 KD DOMAIN (ANION EXCHANGE PF
BINDING DOMAIN).
62 KD DOMAIN (SPECTRIN BINDING
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/FTId=VAR_000601.
D -> N (IN DUESSELDORF).
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/FIId=VAR_000596.
R -> H (IN BRUEGGEN).
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E -> D.
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/FTId-VAR_000599.
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D -> E.
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                                                                                EMBL; X16609; CAA34610.1; -.
EMBL; M28880; AAA51732.1; -.
PIR; S08275; SJHUK.
PIR; A35049; A35049.
HSSP: Q00420; 1AWC.
MIM; 182900; -.
PROSITE: PS50017; DEATH_DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
-i- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
-i- SIMILARITY: CONTAINS 22 ANK REPEATS.
                                                                                                                                                                        ä
                                                                                                                                                                                                          492 NANPNLATTAG-HTPLHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAKYGKVRV 550
                                                                                                                                                                                                                                                                                                          White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
"Mutaine erythrocyte ankytin cDNA: highly conserved regions of the
regulatory domain.";
Mamm. Genome 3:281-285(1992).
-!- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
ELEMENTS: BIND TO THE EXPHROCYTE MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FODENIN, TOBULIN, VIENTIN AND DESMIN.
ERYTHROCYTE ANKYRINS ALSO LINK SPECREIN (BETA CHAIN) TO THE
CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
THEX PETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                      551 AELLLERDAHPNAAGKNGLT-PLHVAVHHNNLDIVKLLLPRGGSP-HSP-AWNGYTPLHI 607
                                                                                                                                                                                                                                      3 EENKGMPSGGGSDEGLATPAR-GLVEKVRHSWEAGADPNGVNRFGRRAIQVMM-GSARV 60
                                                                                                                                                                        Gaps
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PROSITE; PS50017; DEATH_DOMAIN; 1.
PRAS. PF00023; ank; 23.
PFAM; PF00731; death; 1.
PFAM; PF00791; ZUS; 1.
Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
DOMAIN 1827 BKD DOMAIN (ANION EXCHANGE PROTEIN
                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
                                                                                                                                Score 140; DB 1; Length 1880;
Pred. No. 2.39e-08;
25; Mismatches 55; Indels
                                  229 229 A -> S (IN REF. 2).
1245 1545 V -> I (IN REF. 2).
1880 AA; 206145 MW; 1C5FSE7BEDICD428 CRC64;
FTIG-VAR_000602
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANK1_MOUSE STANDARD; PRT; 1862 AA. 202357; 01-NOY-1995 (Rel. 32, Created) 01-NOY-1995 (Rel. 32, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update)
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                                                                                                                              y Match
Local Similarity 32.3%;
hes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
TISSUE-ERYTHROCYTE;
MEDLINE; 92345717.
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119 AEERGHRDVA 128
                                                                                                                                                                                                                                                                                                                                                                608 AAKQNQVEVA 617
                  1698
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                                                        CONFLICT
                                                                                                                                  Query Match
                  VARIANT
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7;
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLUTAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- DEVELOPMENTAL STRAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.

-!- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.

-!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503 LHTAAREGHVDTALALLEKEASQACMTKKGFTPLHVAAKYGKVRLAELLLEHDAHPNAAG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                     SEADING OF ANKRIN (REGULATES THE BINDING OF ANKRIN TO SPECTRIN AND THE BAND 3 PROTEIN).

2 X ANK MOTIF 1.
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       563 KNGLT-PLHVAVHHNNLDIVKLLLPRGGSP-HSP-AWNGYTPLHIAAKQNQIEVA 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
               DOMAIN (SPECTRIN BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 137; DB 1; Length 1862;
Pred. No. 7.81e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     204242 MW; AE6B85B5B29001E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 90385285.
Coffman C., Rarris W., Kintner C.;
"Xotch, the Xanopus homolog of Drosophila notch.";
Science 249:1438-1441(1990).
BINDING DOMAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 2524 AA
              62 KD
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Best Local Similarity 33.9%;
Matches 39; Conservative
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                                                                                       1862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1862 AA;
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               828
                                          1387
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NOTC_XENLA
P21783;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R PIR; A35844; A35844.

R PIR; A35844; A35844.

R RINTS; PROFO10; EGFBLOOD.

R PROSITE; PS00010; ASX_HIDROXYL; 23.

R PROSITE; PS01186; EGF_2; 29.

R PROSITE; PS01187; EGF_CA; 21.

R PROSITE; R PROFO03; EGF; 36.

R PFAM; PF00008; EGF; 36.

R PFAM; PF00006; notch; 3.

W Differentiation; Neurogenesis; Repeat; ANK repeat; EGF-like domain; Transmembrane; Signal; Glycoprotein.
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Lux S.E., Ward D.C., Porget B.G.;
Lux S.E., Ward D.C., Porget B.G.;
ankyrin gene.";
Genomics 10:858-866(1991).
-!- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
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MEDLINE, 91302466.
Otto E., Kunimoto M., McLaughlin T., Bennett V.;
Otto E., Kunimoto M., McLaughlin T., Bennett V.;
"Isolation and characterization of cDNAs encoding human brain ankyrins reveal a family of alternatively spliced genes.";
O. Cell Biol. 114:241-253(1991).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHALN) TO THE CYTOPLASMIC DOMAIN OF THE REYTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

ALTERNATIVE PRODUCTS: THE TWO BRAIN VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICITY: PLASAM MEMBRANE OF NEURONS AS WELL AS GLIAL CELLS THROUGHOUT THE BRAIN.

SIMILARITY: CONTAINS 24 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 131; DB 1; Length 1839;
Pred. No. 8.05e-07;
22; Mismatches 45; Indels
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B39643; B39643.
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Best Local Similarity 32.7%;
Matches 35; Conservative
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PFAM; PF00791; 2U5; 1
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1839 AA;
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524 DAATINGYI-PLHISAREGQVDVASVLLEAGAAHSLAIKKGFIPLHV 569

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Gaps

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Search completed: Thu Jul 20 08:39:16 2000

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:39:33 2000; MasPar time 17.39 Seconds 546.235 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-016-869A-4 (1-137) from US09016869A.pep 977 Description: Perfect Score:

1 MREENKGMPSGGGSDEGLAT.....LAEERGHRDVAGYLRTATGD 137 Sequence:

PAM 150 Gap 11 Scoring table:

225878 seqs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembil2
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_lnvertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 42.547; Variance 77.508; scale 0.549 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ					
Result No.	Score	Query Match	Query Match Length DB	DB	ឧ	Description	Pred. No.
-	598	61.2	86	မ	Q9XS52	P15/MTS2/CDKN2B (FRAGM	3.48e-103
7	586	60.0	115	4	016361	CELL CYCLE NEGATIVE RE	1.61e-100
m	582	59.6	102	ø	09XS51	P16/CDKN2A/MTS1 (FRAGM	1.24e-99
4	574	58.8	168	Ξ	P97510	CYCLIN DEPENDENT KINAS	7.35e-98
S	570	58.3	168	1	089088	CYCLIN DEPENDENT KINAS	5.65e-97
9	563	57.6	86	Ħ	09Z1C1	_	2.00e-95
7	551	56.4	86	Ξ	054846	CYCLIN-DEPENDENT KINAS	8.99e-93
80	479	49.0	113	1	09z1C2	_	5.81e-77
σ	364	37.3	124	13	P70067	CDNK2X PROTEIN.	3.36e-52
10	358	36.6	58	9	9886	CYCLIN-DEPENDENT KINAS	6.26e-51
ส	357	36.5	124	13	Q9W618	P13CDKN2X.	1.02e-50
12	309	31.6	78	7	015125	ALTERNATIVE SPLICED FO	1.14e-40
13	186	19.0	44	Ħ	0921C0	CYCLIN-DEPENDENT KINAS	3.15e-16
14	141	14.4	745	4	09Y544	DJ20208.1 (NOVEL RAT E	3.76e-08
15	140	14.3	1719	4	013768	ALT. ANKYRIN (VARIANT	5.57e-08
16	140	14.3	1856	4	099407	ANKYRIN.	5.57e-08
17	139	14.2	800	'n	043988	HOMEOBOX-CONTAINING PR	8.24e-08
18	139	14.2	837	11	063618	ESPIN.	8.24e-08
19	137	14.0	1098	1	061304	ANKYRIN 1, ERYTHROID (	1.80e-07
20	137	14.0	1848	11	061302	ANKYRIN 1, ERYTHROID (	1.80e-07

136   13.9   251   11   061905   NOTCH PROTEIN HOMOLOG   2.65e-07     135   13.8   843   1   061307   NOTCH PROTEIN HOMOLOG   2.65e-07     135   13.8   812   4   093616   NOTCH PROTEIN HOMOLOG   3.90e-07     135   13.8   1762   1   088521   190 KDA ANKYRIN G  190-07     132   13.8   1762   1   038521   190 KDA ANKYRIN G  150F   3.90e-07     132   13.5   13.8   4   070511   270 KDA ANKYRIN G  150F   3.90e-07     132   13.5   13.4   4   070511   270 KDA ANKYRIN G  150F   3.90e-07     132   13.5   13.4   4   0712955   ANKYRIN G  150F   3.90e-07     131   13.4   119   4   012955   ANKYRIN G  150F   3.90e-07     131   13.4   119   4   012955   ANKYRIN G  150F   3.80e-06     132   13.0   13.1   P07582   ANKYRIN G  150F   3.80e-06     133   13.0   13.1   9.95517   NOTCH-1 (FRAGMENT).   3.80e-06     134   126   12.9   2447   3   013149   NOTCH-4 (FRAGMENT).   1.26e-06     135   13.0   23.1   4   095271   TRF1-INTERACTING ANKYR   1.20e-05     134   12.7   1095   4   09940   NOTCH-4 (FRAGMENT).   2.54e-05     133   12.6   12.9   47   4   096794   NOTCH-2 (FRAGMENT).   3.60e-05     134   12.7   1095   4   099794   NOTCH-2 (FRAGMENT).   3.60e-05     135   12.6   47   4   096794   NOTCH-2 (FRAGMENT).   3.60e-05     134   12.8   12.6   47   4   096794   NOTCH-2 (FRAGMENT).   3.60e-05     134   12.8   12.6   47   4   096794   NOTCH-2 (FRAGMENT).   3.60e-05     135   12.6   12.9   4   096794   NOTCH-2 (FRAGMENT).   3.60e-05     135   12.6   47   4   096794   NOTCH-2 (FRAGMENT).   3.60e-05     135   12.6   47   4   096794   NOTCH-2 (FRAGMENT).   3.60e-05     135   12.6   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   12.9   1
136   13.9   251   11   Q61905   NOTCH PROTEIN HOM
1 136 13.9 251 11 136 13.9 1943 11 135 13.8 682 42 11 135 13.8 13.8 1762 11 135 13.8 13.8 1762 11 132 13.2 13.4 13.4 13.4 13.4 13.4 13.4 13.4 13.4
136 13.9 251 135 135 13.9 1943 135 135 13.8 8883 135 135 13.8 1762 135 135 13.8 1762 132 133 13.8 1762 132 133 13.8 1762 132 133 13.8 1762 123 13.9 1411 124 127 13.0 2321 124 127 13.0 2321 125 126 12.9 2447 127 128 12.6 497
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## ALIGNMENTS

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01-MAY-1999 (TrEMELrel. 03, Created)
01-MAY-1999 (TrEMELrel. 10, Last sequence update)
01-MOY-1999 (TrEMELrel. 10, Last sequence update)
01-NOY-1999 (TrEMELrel. 12, Last annotation update)
CYCLIN DEPENDENT KINASE INHIBITOR PIGINKA (PIGINKA TUMOR SUPPRESSOR
PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (PIG, INHIBITS CDK4)
(PIGINKAA) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-PBMC;
OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
NISHIGAKI K., WATARI T., TSUJIMOTO H., BASEGAWA A.;
"Cloning and chromosomal mapping of the felline genes p16(MTSL/CDKN2A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 QVMMMGSARVAELLILLERGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 QVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VMMMGSARVAELLLLHGADPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                     STONE S., JIANG P., DAYANANTH P., TAVTIGIAN S.V., KATCHER H., PARRY D., PETERS G., KAMB A.;
"Complex structure and regulation of the P16 (MTS1) locus.";
Cancer Res. 55:2988-2994(1995).
EMBL: S78535; AAC60650.1; -.
HSSP; P42771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
P16/CDKN2A/MTS1 (FRAGMENT).
Felis silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 586; DB 4; Length 115;
Pred. No. 1.61e-100;
2; Mismatches 2; Indels
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Pred. No. 1.24e-99;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and p15(WTS2/CDKNZB).";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010807; BAA33540.1; -.
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102 AA; 10824 MW; 8C3094E9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                115 AA; 12334 MW; F5BEF54B CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 WGRLPVDLAEERGHRDVAGYLRTAIG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.0%;
Best Local Similarity 95.3%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.6%;
Best Local Similarity 92.9%;
Matches 79; Conservative
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                                                                                         SEQUENCE FROM N.A. MEDLINE; 95330726.
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SEQUENCE
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P97510
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ID P99
AC P9
DT 011
DT 010
DE CY
DE PF
DE CF
DE CY
CE CF
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MEDLINE; 97179476.
HERZOG C.R., YOU M.;
"Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE OF 1-42 FROM N.A.
STRAIN-DBA/2 AND C57BL/6;
MEDLINE; 95380169.
QUELLE D.E., ASHMUN R.A., HANNON G.J., REHBERGER P.A., TRONO D.,
RICHTER K.H., WALKER C., BEACH D., SHERR C.J., SERRANO M.;
"Cloning and characterization of murine ploink4a and plsink4b genes.";
Oncogene 11:635-645(1995).
                                                                                                  ZHANG S., RAMSAY E.S., MOCK B.A.; "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and p19ARF, is a candidate for the plasmacytoma susceptibility locus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CAST/EI, C57BL/6J AND RF/J, MOLE/EI AND MUS MUS MUSCULUS;
SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 97128829.
SOLOFF E.V., HERZOG C.R., YOU M.;
"The 5'-flanking region of the El alpha form of the murine pl6INK4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J X DBA;
MALDWBRES M., DE CASTRO I., SANTOS J., MELENDEZ B., MANGUES
SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.;
SUBMILLED (JAN-1997) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 574; DB 11; Length 168;
Pred. No. 7.35e-98;
21; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AF044336; AAC08963.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-DBA/2 AND C57BL/6;
GRESSANI K.M., ROLLINS L.A., MILLER M.S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 AA; 17941 MW; 89AD5E62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U49280; AAC00052.1; -.
U66087; AAB39600.1; -.
U66086; AAB39600.1; JOINED.
AF004588; AAB61416.1; -.
                                                                      STRAIN-DBA/2N; TISSUE-SPLEEN;
MEDLINE; 98151529.
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-155 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.8%;
Best Local Similarity 65.0%;
Matches 80; Conservative
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U79628; AAD00226.1;
U79625; AAD00223.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:104738; Cdkn2a.
PFAM; PF00023; ank; 3.
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                                                                                                                                                                                                             STRAIN-VARIOUS STRAINS;
                                                                                                                                                                                               SEQUENCE OF 1-42 FROM
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        suppressor gene.
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EMBL;
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1 VIMMGSAQVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAW 60
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF015460; AAB94534.1; -.
HSSP; 442771; 1B17.
NON_TER 1
SEQUENCE 86 AA; 9237 MW; FEC97F63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GRLPVDLAEEQGHRDIARYLHAASGD 86
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Best Local Similarity 89.5%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinase; Cyclin.
RTA 134
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NON_TER
SEQUENCE
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054846
054846;
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132
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SEQUENCE OF 1-42 FROM N.A.

STRAIN-BALB/CJ AND MUS WOSCHIAVINUS;

SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,

RAMTOS J., MELENDEZ PIQUERAS J.;

"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains.";

In mouse inbred strains.";

EMBL; AFO44335; AAC08962.1;

EMBL; AFO4435; AAC0851.1;

EMBL; JO9626; AAC00051.1;

EMBL; JO9626; AAC00051.1;

REMBL; U9526; AAC00053.1;

REMBL; U9526; AAC00053.1;

REMBL; U9526; AACO0053.1;

REMBL; U9526; AACONOS3.1;

REMBL; U9526; AACON
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                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
02CLIN DEPENDENT KINASE INHIBITOR PIGINK4A (PIGINK4A TUMOR SUPPRESSOR
PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
CDKNZA OR EIALPHA OR P16.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BALLAY, CANNT: TISSUE-SPLEEN;
MEDLINE; 98151529.
ZHANG S., RAMSAY E.S., MOCK B.A.;
"CAKRA, the cyclin-dependent kinase inhibitor encoding pl6INK4a and pl9ARF, is a candidate for the plasmacytoma susceptibility locus, Pctrl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SAADRLARAAAQGRVPDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHIAALLLNYGADS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAADRLARAAAQGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMMGNVHVAALLLNYGADS
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 5.65e-97;
22; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                         168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Best Local Similarity 64.2%;
Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97179476.
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RTA 134
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089088
089088;
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SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M., PERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (CCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79637; AAD00237.1;
HSSP; 942771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                       Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 563; DB 11; Length 86;
Pred. No. 2.00e-95;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NUV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PISINK4B (FRAGMENT).
                  0921C1;
01-MAY-1999 (TIEMBLE). 10, Created)
01-MAY-1999 (TIEMBLE). 10, Last sequence update)
01-NOV-1999 (TIEMBLE). 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
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86 AA.
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1
86 86
86 AA; 9269 MW;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-SPRET/EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-C57BL/6J;
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Score 551; DB 11; Length av; Pred. No. 8.99e-93; Ylematches 2; Indels

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64 TDKSTGATPLHDAARTGFLDTVQLLVKAGADPQARDKDNCLPIDLARQNGHTDVVAVLET 123
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Acanthopterygil; Atherinomorpha;
Cyprinodontiformes; Cyprinodontoidei; Poecillidae; Xiphophorus.
                                                                                              4 EDELTTAAAKGHTAEVEALLLQGAPVNGVNSFGRRAIQVMMGSSEVARLLLTRGADPNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDELTTAAAKGHTAEVEALLLQGAPVNGVNSFGRRAIQVMMMGSSEVARLLLTRGADPNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIEDER S., CHECA-CORTES M.L., JOERG H., STRANZINGER G.;
"An equine sequence homologous to cyclin-dependent kinase inhibitor
(CDKN2A).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 AGADPINGVIRFGRRAIOVMANGSARVAELLILHGAEPINCADPATUTRPVHDAARBGFL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGADPNGVNGFGRRPIQVMAMGSVHVAELLLLHGADPNRADPDTLTRPVHDAAREGFL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEATING SARABIA;
KRAZINETO SARABIA;
KRAZINIS S., MORIZOT D.C., DELLA COLETTA L., JOHNSTON D.A.,
WOOLCOCK B., VIELKIND J.R., NAIRN R.S.;
COMPARATIVE STUDICTURE and Characterization of a CDKNZ Gene:
Xiphophorus Fish Melanoma Model.";
Submitted (WAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF132500; AAD21313.1; --
SERGUENCE 124 AA, 13049 MW; DA386E94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 358; DB 6; Length 58; Pred. No. 6.26e-51; 3; Mismatches 4; Indels
Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF076782; AAC97110.1; ...
HSSP; P42771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE 2A INHIBITOR (FRAGMENT).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   58 A.A.
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                                                                                                                                                                                                                                                                                                                                                                   PRT;
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   19;
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58 AA; 6162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, P13CDKN2X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 36.6%;
Best Local Similarity 87.9%;
Matches 51; Conservative
   63; Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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NON_TER 1
NON_TER 58
SEQUENCE 58 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE-SKIN;
                                                                                                                                                                                                                                                                                                                                      LT 10
097886
097886;
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Q9W6I8
Q9W6I8;
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.;
PELLICER A., FERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79634; ABD00236.1; -.
EMBL: P42771; BIT7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xiphophorus maculatus (Southern platyfish).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Actinopterygil;
Neopterygil; Teleostei; Buteleostei, Acanthopterygil; Atherinomorpha;
Cyprinodontiformes; Cyprinodontoidei; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŚEQUENCE FROM N.A.
STRAIN-JP 163 A; TISSUE-MUSCLE;
MEDLINE; 97075115.
MAIRN R.S., KAZIANIS S., MCENTIRE B.B., DELLA COLETTA L., WALTER R.B.
MORIZOT D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VMMMGNVHVAALLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                               Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 479; DB 11; Length 113
Pred. No: 5.81e-77;
13; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAZIANIS S., NAIRN R.S.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; 069273; ABD9560.3; -.
HSSP; P42771; 1BT7.
SEQUENCE 124 AA; 13034 MW; BFB0B9C5 CRC32;
                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata,
Eutherla, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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Pred. No. 3.36e-52;
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                                                                                                                       113 AA
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112 GRLPVDLAEERGHRDVAGYLRTATGD 137
                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                    P16.
Mus spretus (Western wild mouse).
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112 GRLPVDLAEERGHRDVAGYLRTA 134
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52.5%;
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Best Local Similarity 74.7%;
Matches 62; Conservative
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Best Local Similarity
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SEQUENCE
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116 VDLAEERGHRDVAGYLRT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.4%;
Local Similarity 44.9%;
les 35; Conservative
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Local Similarity 32.3%;
les 42; Conservative
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EMBL; X16609; CAA34611.1;
HSSP; Q00421; IAWC.
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PRELIMINARY;
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TISSUE-HEMATOPOIETIC;
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119 AEERGHRDVA 128
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                                                                                                        64 TDKSTGATPLHDAARTGFLDTVQLLVEAGADPQARDKDNCLPIDLARQNGHTDVVAVLET 123
  Gaps
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MEDLINE: 97373727.
TSUBARI M., TIHONEN E., LAIHO M.;
TSUBARI M., TIHONEN E., LAIHO M.;
"Cloning and characterization of p10, an alternatively spliced in p15 cyclin-dependent kinase inhibitor.";
Cancer Res. 57:2966-2973(1997).
EMBL: AF004619; AAB69899.1; -.
HSSP; P42773; 1BU9.
SEQUENCE 78 AA; 8078 MW; 70693F9A CRC32;
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Mus.
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MREENKGMPSGGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 186; DB 11; Leuy...
Pred. No. 3.15e-16;
.......hoes 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 309; DB 4; Length 78;
Pred. No. 1.14e-40;
3; Mismatches 2; Indels
                                                                                                                                                                                                   O15125 PRELIMINARY; PRT; 78 AA.
O15125,
O1-7AN-1998 (TTEMBLIEL: 05, Created)
O1-JAN-1998 (TTEMBLIEL: 05, Last sequence update)
O1-NOV-1999 (TTEMBLIEL: 12, Last annotation update)
ALTERNATIVE SPLICED FORM OF P15 CDK INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GGSSDAGLATAAARGQVETVRQLLEAGADPNALNRFGRRPIQ 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GGGSDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRAIQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21E6F311 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus spretus (Western wild mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 44
44 AA; 4537 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.7%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 19.0%;
Local Similarity 71.4%;
nes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinase; Cyclin.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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0921C0
0921C0;
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251 GHTKVLSWLLLHGGEIS-ADLWGGT-PLHDAAENGELECCQILVVNGAELDVRDRDGYTA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 NANPNLATTAG-HTPLHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAKYGKVRV 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 90158830.
LUX S.E., JOHN K.M., BENNETI V.;
"Analysis of CDNA for human erythrocyte ankyrin indicates a repeated
structure with homology to tissue-differentiation and cell-cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 EENKGMPSGGSDEGLATPAR-GLVEKVRHSWEAGADPNGVNRFGRRAIQVMMM-GSARV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DJ202001. (NOVEL RAT ESPIN LIKE PROTEIN CONTAINING ANK REPEATS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ALT. ANKYRIN (VARIANT 2.2).
HOMO Saplens (Human).
Eukaryota, Metazoa, Chordata, Cranlata; Vertebrata; Mammalla, Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 140; DB 4; Length 1719;
Pred. No. 5.57e-08;
25; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 141; DB 4; Length 745
Pred. No. 3.76e-08;
12; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                        SECTENCE FROM N.A.
HOWDEN P.;
SUBMILTER (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL031848; CAB46197.1; -.
NON_TER 745 A45
SEQUENCE 745 AA; 78960 MW; FlAB0F4C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00023; ank; 22.
PFAM; PF00531; death; 1.
PFAM; PF00791; ZUS; 1.
SEQUENCE 1719 AA; 189010 MW; CE3D699D CRC32;
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RESULT

Matches

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Search completed: Thu Jul 20 08:39:54 2000 Job time: 21 secs.